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Gallo et al.

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(54) **MOLECULAR CLONING OF HIV-1 FROM IMMORTALIZED CELL LINES**

(75) Inventors: **Robert C. Gallo**, Bethesda, MD (US); **Flossie Wong-Staal**, San Diego, CA (US); **Mikulas Popovic**, Bethesda, MD (US); **Beatrice H. Hahn**, Wallingford, PA (US); **George M. Shaw**, Wallingford, PA (US); **Amanda G. Fisher**, London (GB)

(73) Assignee: **The United States of America as represented by the Secretary, Department of Health and Human Services**, Washington, DC (US)

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Related U.S. Application Data

(63) Continuation of application No. 07/832,603, filed on Feb. 12, 1992, now abandoned, which is a continuation of application No. 07/160,827, filed on Feb. 26, 1988, now abandoned, which is a continuation-in-part of application No. 07/033,891, filed on Apr. 3, 1987, now abandoned, which is a continuation of application No. 06/643,306, filed on Aug. 22, 1984, now abandoned, said application No. 07/160,827 is a continuation-in-part of application No. 06/813,069, filed on Dec. 24, 1985, now abandoned, and a continuation-in-part of application No. 06/693,866, filed on Jan. 23, 1985, which is a continuation-in-part of application No. 06/659,339, filed on Oct. 10, 1984, now abandoned, which is a continuation-in-part of application No. 06/643,306, filed on Aug. 22, 1984, now abandoned.

(51) **Int. Cl.**
C12Q 1/68 (2006.01)
C12Q 1/70 (2006.01)

(52) **U.S. Cl.**
CPC ***C12Q 1/703*** (2013.01); *C12Q 1/6834* (2013.01); *C12Q 1/6876* (2013.01)

(58) **Field of Classification Search**
USPC 435/235, 252.3, 240.2, 172.3, 69.1, 435/236, 320.1, 91, 91.1, 91.32, 91.4; 536/27
See application file for complete search history.

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5,043,262	A		8/1991	Haseltine
5,047,435	A		9/1991	Lavie
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Primary Examiner — Aaron Priest

(74) *Attorney, Agent, or Firm* — Siegfried J. W. Ruppert; Susan S. Rucker

(57) **ABSTRACT**

Disclosed is the molecular cloning of HTLV-III, the adult leukemia and acquired immune deficiency syndrome (AIDS) virus. Clone BH10 contains a 9.0 Kb viral insert constituting the entire HTLV-III genome. Clones BH8 and BH5 contain viral inserts of 5.5 Kb and 3.5 Kb, respectively. These clones are suitable for the development of diagnostic and therapeutic measures for AIDS, as well as use as probes for the detection of AIDS. By scientific convention, HTLV-III, referred to herein also as HIV, has been renamed as HIV-1.

161 Claims, 16 Drawing Sheets

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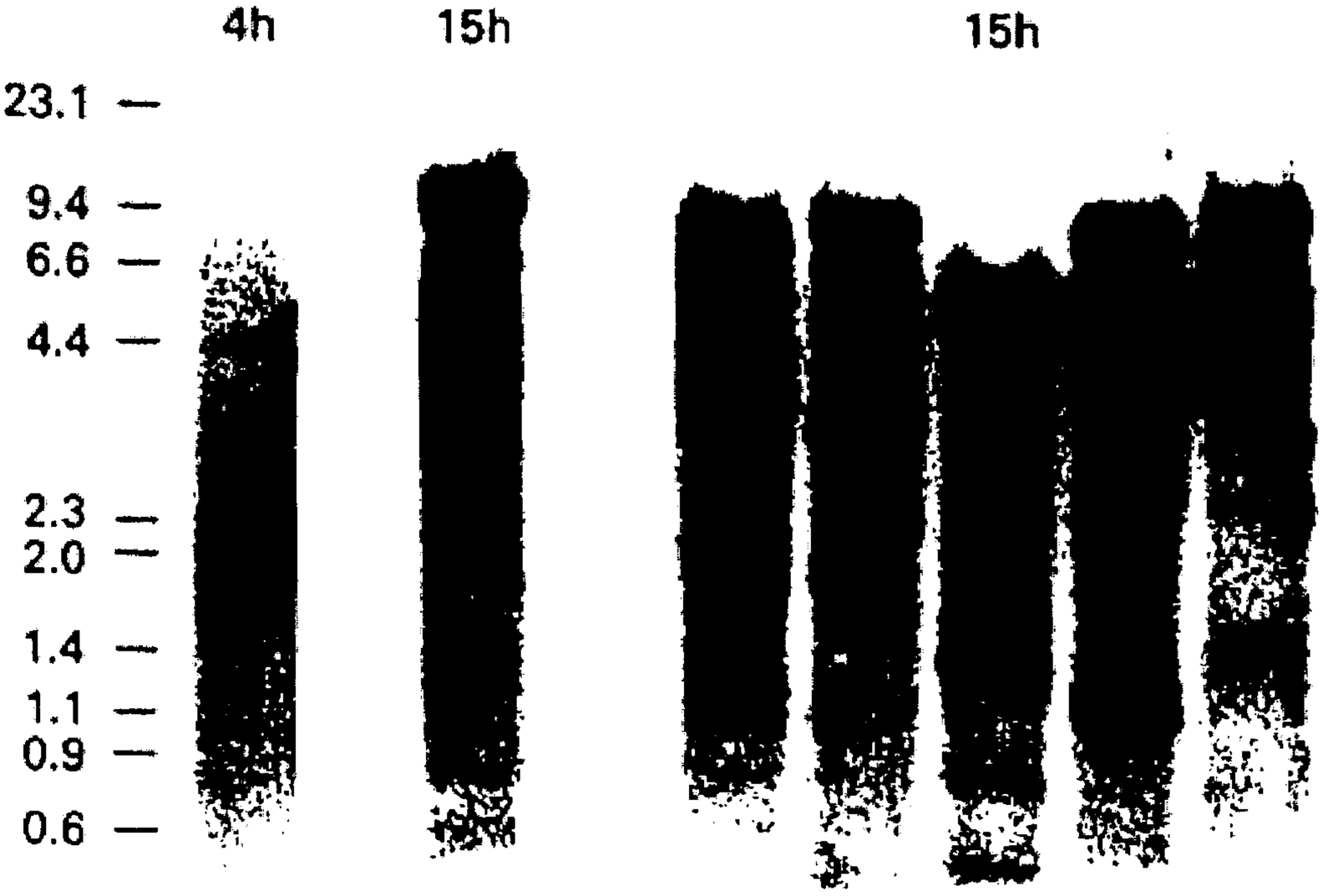
4h
15h
15h
23.1
9.4
6.6
4.4
2.3
2.0
1.4
1.1
0.9
0.6
UNDIGESTED
EcoRI
SstI
HindIII
BamHI
XbaI

FIG. 1

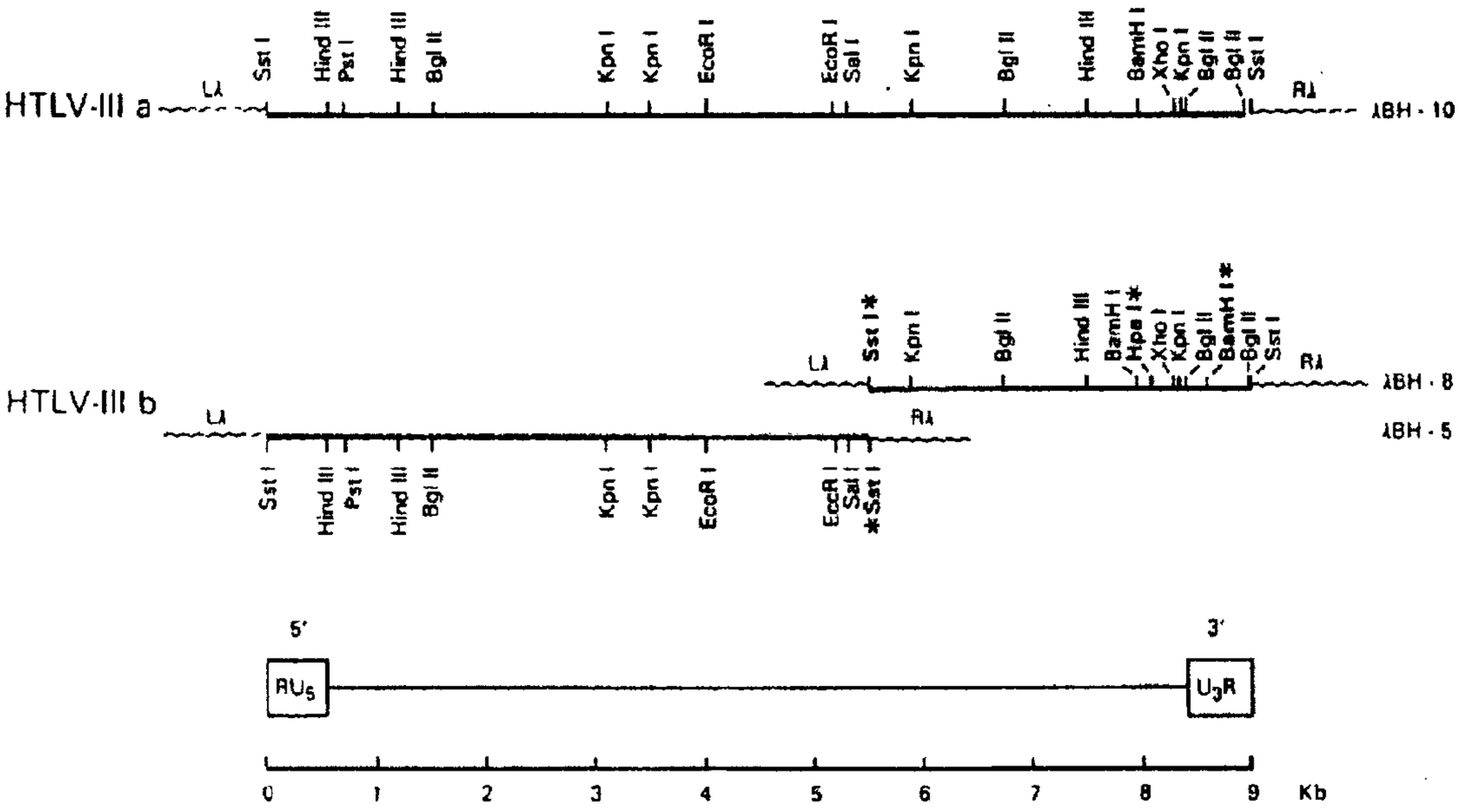
HTLV-III a
LI
Sst I
Hind III
Pst I
Hind III
Bgl II
Kpn I
Kpn I
EcoR I
EcoR I
Sal I
Kpn I
Bgl II
Hind III
BamH I
Xho I
Kpn I
Bgl II
Bgl II
Sst I
RI
λBH - 10
HTLV-III b
LI
Sst I*
Kpn I
Bgl II
Hind III
BamH I
Hpa I*
Xho I
Kpn I
Bgl II
BamH I*
Bgl II
Sst I
RI
λBH - 8
λBH - 5
RI
Sst I
Hind III
Pst I
Hind III
Bgl II
Kpn I
Kpn I
EcoR I
EcoR I
Sal I
*Sst I
5'
3'
RU5
U3R
0
1
2
3
4
5
6
7
8
9
Kb

FIG. 2

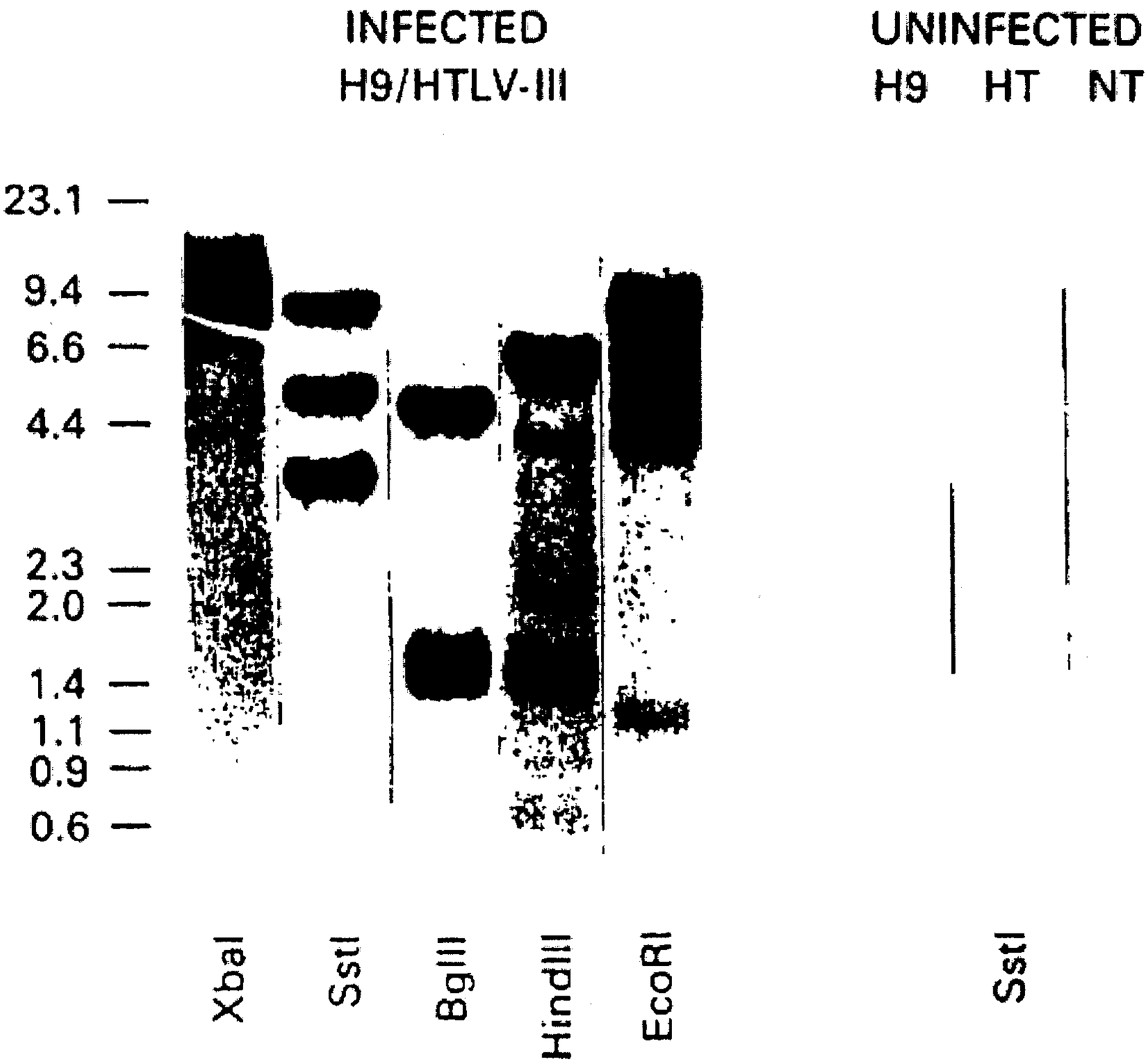
INFECTED
H9/HTLV-III
UNINFECTED
H9 HT NT
23.1
9.4
6.6
4.4
2.3
2.0
1.4
1.1
0.9
0.6
XbaI
SstI
BglII
HindIII
EcoRI
SstI

FIG. 3

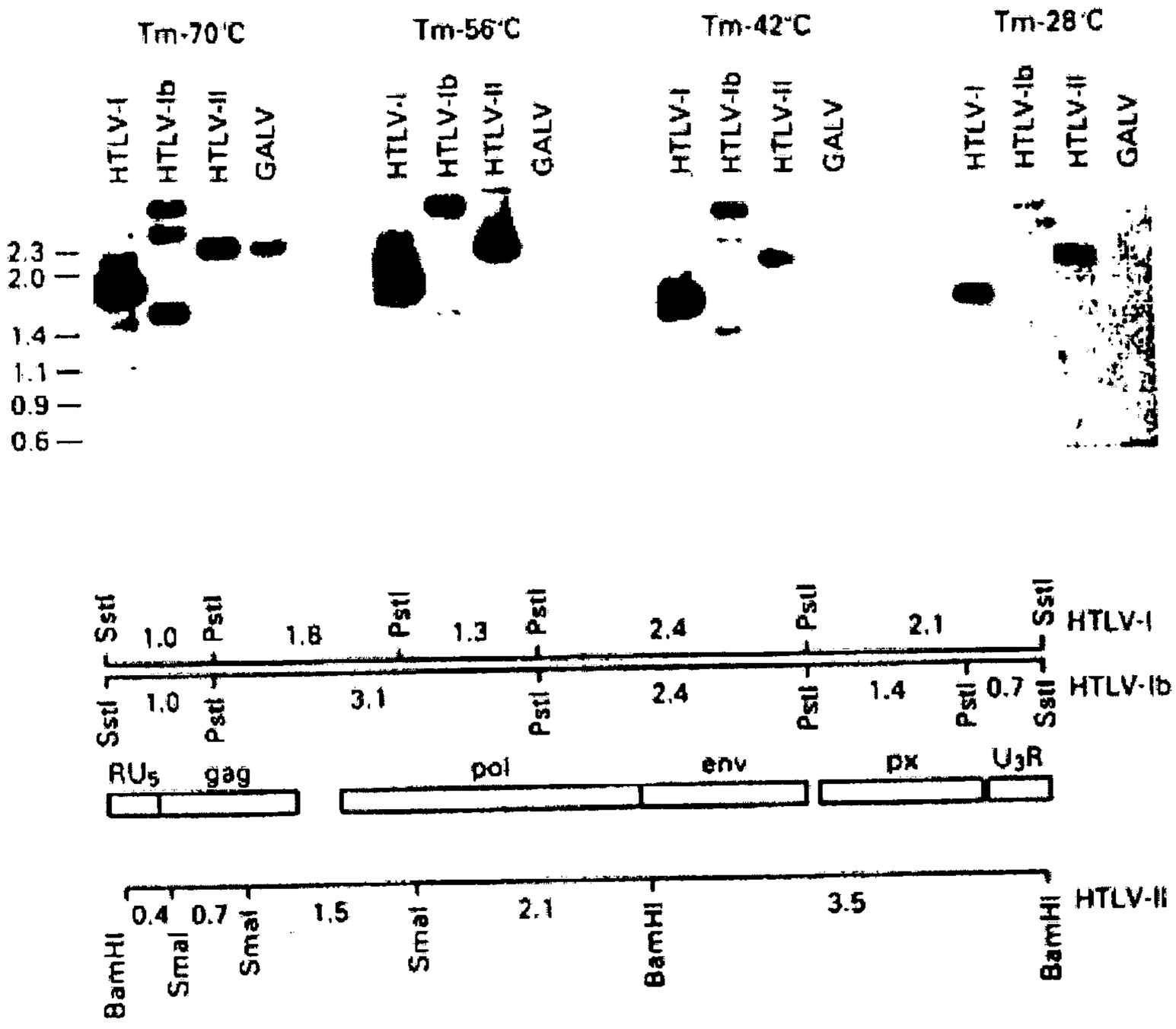
Tm-70°C
Tm-56°C
Tm-42°C
Tm-28°C
HTLV-I
HTLV-Ib
HTLV-II
GALV
2.3
2.0
1.4
1.1
0.9
0.6
SstI
PstI
SmaI
BamHI
1.0
1.8
1.3
2.4
2.1
3.1
1.4
0.7
0.4
1.5
2.1
3.5
RU5
gag
pol
env
px
U3R

FIG. 4

GAGCTCTCTCGACGCAGGACTCGGCTTGCTGAAGCGCGCACGGCAAGAGGCGAGGGGCGG 60
CGACTGGTGAGTACGCCAAAAATTTTGACTAGCGGAGGCTAGAAGGAGAGAGATGGGTGC 120
GAGAGCGTCAGTATTAAGCGGGGGAGAATTAGATCGATGGGAAAAAATTCGGTTAAGGCC 180
AGGGGGAAAGAAAAAATATAAATTAAAACATATAGTATGGGCAAGCAGGGAGCTAGAACG 240
ATTCGCAGTTAATCCTGGCCTGTTAGAAACATCAGAAGGCTGTAGACAAATACTGGGACA 300
GCTACAACCATCCCTTCAGACAGGATCAGAAGAACTTAGATCATTATATAATACAGTAGC 360
AACCCTCTATTGTGTGCATCAAAGGATAGAGATAAAAGACACCAAGGAAGCTTTAGACAA 420
GATAGAGGAAGAGCAAAACAAAAGTAAGAAAAAAGCACAGCAAGCAGCAGCTGACACAGG 480
ACACAGCAGTCAGGTCAGCCAAAATTACCCTATAGTGCAGAACATCCAGGGGCAAATGGT 540
ACATCAGGCCATATCACCTAGAACTTTAAATGCATGGGTAAAAGTAGTAGAAGAGAAGGC 600
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TTTAAACACCATGCTAAACACAGTGGGGGGACATCAAGCAGCCATGCAAATGTTAAAAGA 720
GACCATCAATGAGGAAGCTGCAGAATGGGATAGAGTGCATCCAGTGCATGCAGGGCCTAT 780
CGCACCAGGCCAGATGAGAGAACCAAGGGGAAGTGACATAGCAGGAACTACTAGTACCCT 840
TCAGGAACAAATAGGATGGATGACAAATAATCCACCTATCCCAGTAGGAGAAATTTATAA 900
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GGACATAAGACAAGGACCAAAGGAACCCTTTAGAGACTATGTAGACCGGTTCTATAAAAC 1020
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CCAAAATGCGAACCCAGATTGTAAGACTATTTTAAAAGCATTGGGACCAGCAGCTACTCT 1140
AGAAGAAATGATGACAGCATGTCAGGGAGTGGGAGGACCCGGCCATAAAGCAAGAGTTTT 1200
GGCTGAAGCAATGAGCCAAGTAACAAATTCAACTACCATAATGATGCAAAGAGGCAATTT 1260
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CAGACCAGAGCCAACAGCCCCACCAGAAGAGAGCTTCAGGTCTGGGGTAGAGACAACAAC 1560
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TTAGATACAGGAGCAGATGATACAGTATTAGAAGAAATGAGTTTGCCAGGAAGATGGAAA 1740
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ATAGAAATCTGTGGACATAAAGCTATAGGTACAGTATTAGTAGGACCTACACCTGTCAAC 1860
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CCATTGACAGAAGAAAAAATAAAAGCATTAGTAGAAATTTGTACAGAAATGGAAAAGGAA 2040
GGGAAAATTTCAAAAATTGGGCCTGAAAATCCATACAATACTCCAGTATTTGCCATAAAG 2100

FIG. 5

AAAAAAGACAGTACTAAATGGAGAAAATTAGTAGATTTCAGAGAACTTAATAGGAGAACT 2160
CAAGACTTCTGGGAAGTTCAATTGGGAATACCACATCCCGCAGGGTTAAAAAAGAAAAAA 2220
TCAGTAACAGTACTGGATGTGGGTGATGCATATTTTTCAGTTCCCTTAGATGAAGACTTC 2280
AGGAAGTATACTGCATTTACCATACCTAGTATAAATAATGAGACACCAGGGATTAGATAT 2340
CAGTACAATGTGCTTCCACAGGGATGGAAAGGATCACCAGCAATATTCCAAAGTAGCATG 2400
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FIG. 5 (continued)

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CAGGATGAGGATTAGAACATGGAAAAGTTTAGTAAAACACCATATGTATGTTTCAGGGAA 4500

AGCTAGGGGATGGTTTTATAGACATCACTATGAAAGCCCTCATCCAAGAATAAGTTCAGA 4560

AGTACACATCCCACTAGGGGATGCTAGATTGGTAATAACAACATATTGGGGTCTGCATAC 4620

AGGAGAAAGAGACTGGCATTTGGGTCAGGGAGTCTCCATAGAATGGAGGAAAAGGAGATA 4680

TAGCACACAAGTAGACCCTGAACTAGCAGACCAACTAATTCATCTGTATTACTTTGATTG 4740

TTTTTCAGACTCTGCTATAAGAAAGGCCTTATTAGGACACATAGTTAGCCCTAGGTGTGA 4800

ATATCAAGCAGGACATAACAAGGTAGGATCTCTACAATACTTGGCACTAGCAGCATTAAT 4860

AACACCAAAAAAGGGAAAGCCACCTTTGCCTAGTGTTACGAAACTGACAGAGGATAGATG 4920

GAACAAGCCCCAGAAGACCAAGGGCCACAGAGGGAGCCACACAATGAATGGACACTAGAG 4980

CTTTTAGAGGAGCTTAAGAATGAAGCTGTTAGACATTTTCCTAGGATTTGGCTCCATGGC 5040

TTAGGGCAACATATCTATGAAACTTATGGGGATACTTGGGCAGGAGTGGAAGCCATAATA 5100

AGAATTCTGCAACAACTGCTGTTTATCCATTTTCAGAATTGGGTGTCGACATAGCAGAAT 5160

AGGCGTTACTCAACAGAGGAGAGCAAGAAATGGAGCCAGTAGATCCTAGACTAGAGCCCT 5220

GGAAGCATCCAGGAAGTCAGCCTAAAACTGCTTGTACCACTTGCTATTGTAAAAAGTGTT 5280

GCTTTCATTGCCAAGTTTGTTTCATAACAAAAGCCTTAGGCATCTCCTATGGCAGGAAGA 5340

AGCGGAGACAGCGACGAAGAGCTC

FIG. 5 (continued)

```
TGGAAGGGCTAATTCACTCCCAACGAAGACAAGATATCCTTGATCTGTGGATCCACCACA      60
CACAAGGCTACTTCCCTGATTGGCAGAACTACACACCAGGGCCAGGAGTCAGATATCCAC     120
TGACCTTTGGATGGTGCTACAAGCTAGTACCAGTTGAGCCAGAGAAGTAAGAAGAAGCCA     180
ATAAAGGAGAGAACACCAGCTTGTTACACCCTGTGAGCCTGCATGGAATTGATGACCCGG     240
AGAGAGAAGTGTTAGAGTGGAGGTTTGACAGCCGCCTAGCATTTCATCACATGGCCCGAG     300
AGCTGCATCCGGAGTACTTCAAGAACTGCTGACATCGAGCTTGCTACAAGGGACTTTCCG     360
CTGGGGACTTTCCAGGGAGGCGTGGCCTGGGCGGGACTGGGGAGTGGCGAGCCCTCAGAT     420
CCTGCATATAAGCAGCTGCTTTTTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGA     480
GCCTGGGAGCTCGAGCTCATCGAAGCAGTCAGACTCATCAAGTTTCTCTATCAAAGCAGT     540
AAGTAGTACATGTAATGCAACCTATACAAATAGCAATAGTAGCATTAGTAGTAGCAATAA     600
TAATAGCAATAGTTGTGTGGTCCATAGTAATCATAGAATATAGGAAAATATTAAGACAAA     660
GAAAAATAGACAGGTTAATTGATAGACTAATAGAAAGAGCAGAAGACAGTGGCAATGAGA     720
GTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCACCATGCTCCTT     780
GGGATGTTGATGATCTGTAGTGCTACAGAAAAATTGTGGGTCACAGTCTATTTAGGGGTA     840
CCTGTGTGGAAGGAAGCAACCACCACTCTATTTTGTGCATCAGATGCTAAAGCATATGAT     900
ACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCCCAACCCACAA     960
GAAGTAGTATTGGTAAATGTGACAGAAAATTTTAACATGTGGAAAAATGACATGGTAGAA    1020
CAGATGCATGAGGATATAATCAGTTTATGGGATCAAAGCCTAAAGCCATGTGTAAAATTA    1080
ACCCCACTCTGTGTTAGTTTAAAGTGCACTGATTTGAAGAATGATACTAATACCAATAGT    1140
AGTAGCGGGAGAATGATAATGGAGAAAGGAGAGATAAAAAACTGCTCTTTCAATATCAGC    1200
ACAAGCAAAAGAGGTAAGGTGCAGAAAGAATATGCATTTTTTTATAAACTTGATATAATA    1260
CCAATAGATAATGATACTACCAGCTATACGTTGACAAGTTGTAACACCTCAGTCATTACA    1320
CAGGCCTGTCCAAAGGTATCCTTTGAGCCAATTCCCATACATTATTGTGCCCCGGCTGGT    1380
TTTGCGATTCTAAAATGTAATAATAAGACGTTCAATGGAACAGGACCATGTACAAATGTC    1440
AGCACAGTACAATGTACACATGGAATTAGGCCAGTAGTATCAACTCAACTGCTGTTAAAT    1500
GGCAGTCTAGCAGAAGAAGAGGTAGTAATTAGATCTGTCAATTTCACGGACAATGCTAAA    1560
ACCATAATAGTACAGCTGAACACATCTGTAGAAATTAATTGTACAAGACCCAACAACAAT    1620
ACAAGAAAAAGTATCCAAATCCAGAGGGGACCAGGGAGAGCATTTGTTACAATAGGAAAA    1680
ATAGGAAATATGAGACAAGCACATTGTAACATTAGTAGAGCAAAATGGAATGCCACTTTA    1740
AAACAGATAGATAGCAAATTAAGAGAACAATTTGGAAATAATAAAACAATAATCTTTAAG    1800
CAGTCCTCAGGAGGGGACCCAGAAATTGTAACGCACAGTTTTAATTGTGGAGGGGAATTT    1860
TTCTACTGTAATTCAACACAACTGTTTAATAGTACTTGGAGTACTAAAGGGTCAAATAAC    1920
ACTGAAGGAAGTGACACAATCACCCTCCCATGCAGAATAAAACAAATTATAAACATGTGG    1980
CAGGAAGTAGGAAAAGCAATGTATGCCCCTCCCATCAGTGGACAAATTAGATGTTCATCA    2040
AATATTACAGGGCTGCTATTAACAAGAGATGGTGGTAATAGCAACAATGAGTCCGAGATC    2100
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FIG. 6

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TTCAGACCTGGAGGAGGAGATATGAGGGACAATTGGAGAAGTGAATTATATAAATATAAA   2160
GTAGTAAAAATTGAACCATTAGGAGTAGCACCCACCAAGGCAAAGAGAAGAGTGGTGCAG   2220
AGAGAAAAAAGAGCAGTGGGAATAGGAGCTTTGTTCCTTGGGTTCTTGGGAGCAGCAGGA   2280
AGCACTATGGGCGCAGCGTCAATGACGCTGACGGTACAGGCCAGACAATTATTGTCTGGT   2340
ATAGTGCAGCAGCAGAACAATTTGCTGAGGGCTATTGAGGGCCAACAGCATCTGTTGCAA   2400
CTCACAGTCTGGGGCATCAGCAGCTCCAGGCAAGAATCCTGGCTGTGGAAAGATACCTAA   2460
AGGATCAACAGCTCCTGGGGATTTGGGGTTGCTCTGGAAAACTCATTTGCACCACTGCTG   2520
TGCCTTGGAATGCTAGTTGGAGTAATAAATCTCTGGAACAGATTTGGAATAACATGACCT   2580
GGATGGAGTGGGACAGAGAAATTAACAATTACACAAGCTTAATACACTCCTTAATTGAAG   2640
AATCGCAAAACCAGCAAGAAAAGAATGAACAAGAATTATTGGAATTAGATAAATGGGCAA   2700
GTTTGTGGAATTGGTTTAACATAACAAATTGGCTGTGGTATATAAAATTATTCATAATGA   2760
TAGTAGGAGGCTTGGTAGGTTTAAGAATAGTTTTTGCTGTACTTTCTATAGTGAATAGAG   2820
TTAGGCAGGGATATTCACCATTATCGTTTCAGACCCACCTCCCAAACCCGAGGGGACCCG   2880
ACAGGCCCGAAGGAATAGAAGAAGAAGGTGGAGAGAGAGACAGAGACAGATCCATTCGAT   2940
TAGTGAACGGATCCTTAGCACTTATCTGGGACGATCTGCGGAGCCTGTGCCTCTTCAGCT   3000
ACCACCGCTTGAGAGACTTACTCTTGATTGTAACGAGGATTGTGGAACTTCTGGGACGCA   3060
GGGGGTGGGAAGCCCTCAAATATTGGTGGAATCTCCTACAGTATTGGAGTCAGGAACTAA   3120
AGAATAGTGCTGTTAACTTGCTCAATGCCACAGCCATAGCAGTAGCTGAGGGGACAGATA   3180
GGGTTATAGAAGTATTACAAGCAGCTTATAGAGCCATTCGCCACATACCTAGAAGAATAA   3240
GACAGGGCTTGGAAAGGATTTTGCTATAAGATGGGTGGCAAGTGGTCAAAAAGTAGTGTG   3300
GTTGGATGGCCTGCTGTAAGGGAAAGAATGAGACGAGCTGAGCCAGCAGCAGATGGGGTG   3360
GGAGCAGTATCTCGAGACCTAGAAAAACATGGAGCAATCACAAGTAGCAATACAGCAGCT   3420
ACCAATGCTGATTGTGCTTGGCTAGAAGCACAAGAGGAGGAGGAGGTGGGTTTTCCAGTC   3480
ACACCTCAGGTACCTTTAAGACCAATGACTTACAAGGCAGCTGTAGATCTTAGCCACTTT   3540
TTAAAAGAAAAGGGGGGACTGGAAGGGCTAATTCACTCCCAACGAAGACAAGATATCCTT   3600
GATCTGTGGATCCACCACACACAAGGCTACTTCCCTGATTGGCAGAACTACACACCAGGG   3660
CCAGGGATCAGATATCCACTGACCTTTGGATGGTGCTACAAGCTAGTACCAGTTGAGCCA   3720
GAGAAGATAGAAGAAGCCAATAAAGGAGAGAACACCAGCTTGTTACACCCTGTGAGCCTG   3780
CATGGGATGGATGACCCTGAGAGAGAAGTGTTAGAGTGGAGGTTTGACAGCCGCCTAGCA   3840
TTTCATCACATGGCCCGAGAGCTGCATCCGGAGTACTTCAAGAACTGCTGACATCGAGCT   3900
TGCTACAAGGGACTTTCCGCTGGGGACTTTGCGTGGCCTGGGCGGGACTGGGGAGTGGCG   3960
AGCCCTCAGATCCTGCATATAATTTTTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATC   4020
TGAGCCTGGGAGCTC
```

FIG. 6 (continued)

```
TGGAAGGGCTAATTCACTCCCAACGAAGACAAGATATCCTTGATCTGTGGATCTACCACA      60
CACAAGGCTACTTCCCTGATTAGCAGAACTACACACCAGGGCCAGGGATCAGATATCCAC     120
TGACCTTTGGATGGTGCTACAAGCTAGTACCAGTTGAGCCAGAGAAGTTAGAAGAAGCCA     280
ACAAAGGAGAGAACACCAGCTTGTTACACCCTGTGAGCCTGCATGGAATGGATGACCCGG     240
AGAGAGAAGTGTTAGAGTGGAGGTTTGACAGCCGCCTAGCATTTCATCACATGGCCCGAG     300
AGCTGCATCCGGAGTACTTCAAGAACTGCTGACATCGAGCTTGCTACAAGGGACTTTCCG     360
CTGGGGACTTTCCAGGGAGGCGTGGCCTGGGCGGGACTGGGGAGTGGCGAGCCCTCAGAT     420
CCTGCATATAAGCAGCTGCTTTTTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGA     480
GCCTGGGAGCTCGAGCTCTCTCGACGCAGGACTCGGCTTGCTGAAGCGCGCACGGCAAGA     540
GGCGAGGGGCGGCGACTGGTGAGTACGCCAAAAATTTTGACTAGCGGAGGCTAGAAGGAG     600
AGAGATGGGTGCGAGAGCGTCAGTATTAAGCGGGGGAGAATTAGATCGATGGGAAAAAAT     660
TCGGTTAAGGCCAGGGGGAAAGAAAAAATATAAATTAAAACATATAGTATGGGCAAGCAG     720
GGAGCTAGAACGATTCGCAGTTAATCCTGGCCTGTTAGAAACATCAGAAGGCTGTAGACA     780
AATACTGGGACAGCTACAACCATCCCTTCAGACAGGATCAGAAGAACTTAGATCATTATA     840
TAATACAGTAGCAACCCTCTATTGTGTGCATCAAAGGATAGAGATAAAAGACACCAAGGA     900
AGCTTTAGACAAGATAGAGGAAGAGCAAAACAAAAGTAAGAAAAAAGCACAGCAAGCAGC     960
AGCTGACACAGGACACAGCAGTCAGGTCAGCCAAAATTACCCTATAGTGCAGAACATCCA    1020
GGGGCAAATGGTACATCAGGCCATATCACCTAGAACTTTAAATGCATGGGTAAAAGTAGT    1080
AGAAGAGAAGGCTTTCAGCCCAGAAGTAATACCCATGTTTTCAGCATTATCAGAAGGAGC    1140
CACCCCACAAGATTTAAACACCATGCTAAACACAGTGGGGGGACATCAAGCAGCCATGCA    1200
AATGTTAAAAGAGACCATCAATGAGGAAGCTGCAGAATGGGATAGAGTACATCCAGTGCA    1260
TGCAGGGCCTATTGCACCAGGCCAGATGAGAGAACCAAGGGGAAGTGACATAGCAGGAAC    1320
TACTAGTACCCTTCAGGAACAAATAGGATGGATGACAAATAATCCACCTATCCCAGTAGG    1440
AGAAATTTATAAAAGATGGATAATCCTGGGATTAAATAAAATAGTAAGAATGTATAGCCC    1500
TACCAGCATTCTGGACATAAGACAAGGACCAAAAGAACCTTTTAGAGACTATGTAGACCG    1560
GTTCTATAAAACTCTAAGAGCCGAGCAAGCTTCACAGGAGGTAAAAAATTGGATGACAGA    1620
AACCTTGTTGGTCCAAAATGCGAACCCAGATTGTAAGACTATTTTAAAAGCATTGGGACC    1680
AGCGGCTACACTAGAAGAAATGATGACAGCATGTCAGGGAGTAGGAGGACCCGGCCATAA    1740
GGCAAGAGTTTTGGCTGAAGCAATGAGCCAAGTAACAAATACAGCTACCATAATGATGCA    1800
GAGAGGCAATTTTAGGAACCAAAGAAAGATGGTTAAGTGTTTCAATTGTGGCAAAGAAGG    1860
GCACACAGCCAGAAATTGCAGGGCCCCTAGGAAAAAGGGCTGTTGGAAATGTGGAAAGGA    1920
AGGACACCAAATGAAAGATTGTACTGAGAGACAGGCTAATTTTTTAGGGAAGATCTGGCC    1980
TTCCTACAAGGGAAGGCCAGGGAATTTTCTTCAGAGCAGACCAGAGCCAACAGCCCCACC    2040
ATTTCTTCAGAGCAGACCAGAGCCAACAGCCCCACCAGAAGAGAGCTTCAGGTCTGGGGT    2100
AGAGACAACAACTCCCCCTCAGAAGCAGGAGCCGATAGACAAGGAACTGTATCCTTTAAC    2160
```

FIG. 7

```
TTCCCTCAGATCACTCTTTGGCAACGACCCCTCGTCACAATAAAGATAGGGGGGCAACTA    2220
AAGGAAGCTCTATTAGATACAGGAGCAGATGATACAGTATTAGAAGAAATGAGTTTGCCA    2280
GGAAGATGGAAACCAAAAATGATAGGGGGAATTGGAGGTTTTATCAAAGTAAGACAGTAT    2340
GATCAGATACTCATAGAAATCTGTGGACATAAAGCTATAGGTACAGTATTAGTAGGACCT    2400
ACACCTGTCAACATAATTGGAAGAAATCTGTTGACTCAGATTGGTTGCACTTTAAATTTT    2460
CCCATTAGCCCTATTGAGACTGTACCAGTAAAATTAAAGCCAGGAATGGATGGCCCAAAA    2520
GTTAAACAATGGCCATTGACAGAAGAAAAAATAAAAGCATTAGTAGAAATTTGTACAGAA    2580
ATGGAAAAGGAAGGGAAAATTTCAAAAATTGGGCCTGAGAATCCATACAATACTCCAGTA    2640
TTTGCCATAAAGAAAAAAGACAGTACTAAATGGAGAAAATTAGTAGATTTCAGAGAACTT    2700
AATAAGAGAACTCAAGACTTCTGGGAAGTTCAATTAGGAATACCACATCCCGCAGGGTTA    2760
AAAAAGAAAAAATCAGTAACAGTACTGGATGTGGGTGATGCATATTTTTCAGTTCCCTTA    2820
GATGAAGACTTCAGGAAGTATACTGCATTTACCATACCTAGTATAAACAATGAGACACCA    2880
GGGATTAGATATCAGTACAATGTGCTTCCACAGGGATGGAAAGGATCACCAGCAATATTC    2940
CAAAGTAGCATGACAAAAATCTTAGAGCCTTTTAAAAAACAAAATCCAGACATAGTTATC    3000
TATCAATACATGGATGATTTGTATGTAGGATCTGACTTAGAAATAGGGCAGCATAGAACA    3060
AAAATAGAGGAGCTGAGACAACATCTGTTGAGGTGGGGACTTACCACACCAGACAAAAAA    3120
CATCAGAAAGAACCTCCATTCCTTTGGATGGGTTATGAACTCCATCCTGATAAATGGACA    3180
GTACAGCCTATAGTGCTGCCAGAAAAAGACAGCTGGACTGTCAATGACATACAGAAGTTA    3240
GTGGGGAAATTGAATTGGGCAAGTCAGATTTACCCAGGGATTAAAGTAAGGCAATTATGT    3300
AAACTCCTTAGAGGAACCAAAGCACTAACAGAAGTAATACCACTAACAGAAGAAGCAGAG    3360
CTAGAACTGGCAGAAAACAGAGAGATTCTAAAAGAACCAGTACATGGAGTGTATTATGAC    3420
CCATCAAAAGACTTAATAGCAGAAATACAGAAGCAGGGGCAAGGCCAATGGACATATCAA    3480
ATTTATCAAGAGCCATTTAAAAATCTGAAAACAGGAAAATATGCAAGAATGAGGGGTGCC    3540
CACACTAATGATGTAAAACAATTAACAGAGGCAGTGCAAAAAATAACCACAGAAAGCATA    3600
GTAATATGGGGAAAGACTCCTAAATTTAAACTACCCATACAAAAGGAAACATGGGAAACA    3600
TGGTGGACAGAGTATTGGCAAGCCACCTGGATTCCTGAGTGGGAGTTTGTTAATACCCCT    3660
CCTTTAGTGAAATTATGGTACCAGTTAGAGAAAGAACCCATAGTAGGAGCAGAAACCTTC    3720
TATGTAGATGGGGCAGCTAACAGGGAGACTAAATTAGGAAAAGCAGGATATGTTACTAAC    3780
AAAGGAAGACAAAAGGTTGTCCCCCTAACTAACACAACAAATCAGAAAACTGAGTTACAA    3840
GCAATTTATCTAGCTTTGCAGGATTCAGGATTAGAAGTAAACATAGTAACAGACTCACAA    3900
TATGCATTAGGAATCATTCAAGCACAACCAGATAAAAGTGAATCAGAGTTAGTCAATCAA    3960
ATAATAGAGCAGTTAATAAAAAAGGAAAAGGTCTATCTGGCATGGGTACCAGCACACAAA    4020
GGAATTGGAGGAAATGAACAAGTAGATAAATTAGTCAGTGCTGGAATCAGGAAAATACTA    4080
TTTTTAGATGGAATAGATAAGGCCCAAGATGAACATGAGAAATATCACAGTAATTGGAGA    4140
GCAATGGCTAGTGATTTTAACCTGCCACCTGTAGTAGCAAAAGAAATAGTAGCCAGCTGT    4200
GATAAATGTCAGCTAAAAGGAGAAGCCATGCATGGACAAGTAGACTGTAGTCCAGGAATA    4260
```

FIG. 7 (continued)

```
TGGCAACTAGATTGTACACATTTAGAAGGAAAAGTTATCCTGGTAGCAGTTCATGTAGCC      4320
AGTGGATATATAGAAGCAGAAGTTATTCCAGCAGAAACAGGGCAGGAAACAGCATATTTT      4380
CTTTTAAAATTAGCAGGAAGATGGCCAGTAAAAACAATACATACAGACAATGGCAGCAAT      4440
TTCACCAGTGCTACGGTTAAGGCCGCCTGTTGGTGGGCGGGAATCAAGCAGGAATTTGGA      4500
ATTCCCTACAATCCCCAAAGTCAAGGAGTAGTAGAATCTATGAATAAAGAATTAAAGAAA      4560
ATTATAGGACAGGTAAGAGATCAGGCTGAACATCTTAAGACAGCAGTACAAATGGCAGTA      4620
TTCATCCACAATTTTAAAAGAAAAGGGGGGATTGGGGGGTACAGTGCAGGGGAAAGAATA      4680
GTAGACATAATAGCAACAGACATACAAACTAAAGAATTACAAAAACAAATTACAAAAATT      4740
CAAAATTTTCGGGTTTATTACAGGGACAGCAGAAATCCACTTTGGAAAGGACCAGCAAAG      4800
CTCCTCTGGAAAGGTGAAGGGGCAGTAGTAATACAAGATAATAGTGACATAAAAGTAGTG      4860
CCAAGAAGAAAAGCAAAGATCATTAGGGATTATGGAAAACAGATGGCAGGTGATGATTGT      4920
GTGGCAAGTAGACAGGATGAGGATTAGAACATGGAAAAGTTTAGTAAAACACCATATGTA      4980
TGTTTCAGGGAAAGCTAGGGGATGGTTTTATAGACATCACTATGAAAGCCCTCATCCAAG      5040
AATAAGTTCAGAAGTACACATCCCACTAGGGGATGCTAGATTGGTAATAACAACATATTG      5100
GGGTCTGCATACAGGAGAAAGAGACTGGCATTTGGGTCAGGGAGTCTCCATAGAATGGAG      5160
GAAAAAGAGATATAGCACACAAGTAGACCCTGAACTAGCAGACCAACTAATTCATCTGTA      5220
TTACTTTGACTGTTTTTCAGACTCTGCTATAAGAAAGGCCTTATTAGGACACATAGTTAG      5280
CCCTAGGTGTGAATATCAAGCAGGACATAACAAGGTAGGATCTCTACAATACTTGGCACT      5340
AGCAGCATTAATAACACCAAAAAAGATAAAGCCACCTTTGCCTAGTGTTACGAAACTGAC      5400
AGAGGATAGATGGAACAAGCCCCAGAAGACCAAGGGCCACAGAGGGAGCCACACAATGAA      5460
TGGACACTAGAGCTTTTAGAGGAGCTTAAGAATGAAGCTGTTAGACATTTTCCTAGGATT      5520
TGGCTCCATGGCTTAGGGCAACATATCTATGAAACTTATGGGGATACTTGGGCAGGAGTG      5580
GAAGCCATAATAAGAATTCTGCAACAACTGCTGTTTATCCATTTTCAGAATTGGGTGTCG      5640
ACATAGCAGAATAGGCGTTACTCGACAGAGGAGAGCAAGAAATGGAGCCAGTAGATCCTA      5700
GACTAGAGCCCTGGAAGCATCCAGGAAGTCAGCCTAAAACTGCTTGTACCAATTGCTATT      5760
GTAAAAAGTGTTGCTTTCATTGCCAAGTTTGTTTCATAACAAAAGCCTTAGGCATCTCCT      5820
ATGGCAGGAAGAAGCGGAGACAGCGACGAAGACCTCCTCAAGGCAGTCAGACTCATCAAG      5880
TTTCTCTATCAAAGCAGTAAGTAGTACATGTAATGCAACCTATACAAATAGCAATAGTAG      5940
CATTAGTAGTAGCAATAATAATAGCAATAGTTGTGTGGTCCATAGTAATCATAGAATATA      6000
GGAAAATATTAAGACAAAGAAAAATAGACAGGTTAATTGATAGACTAATAGAAAGAGCAG      6060
AAGACAGTGGCAATGAGAGTGAAGGAGAAATATCAGCACTTGTGGAGATGGGGGTGGAGA      6120
TGGGGCACCATGCTCCTTGGGATGTTGATGATCTGTAGTGCTACAGAAAAATTGTGGGTC      6180
ACAGTCTATTATGGGGTACCTGTGTGGAAGGAAGCAACCACCACTCTATTTTGTGCATCA      6240
GATGCTAAAGCATATGATACAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCC      6300
ACAGACCCCAACCCACAAGAAGTAGTATTGGTAAATGTGACAGAAAATTTTAACATGTGG      6360
AAAAATGACATGGTAGAACAGATGCATGAGGATATAATCAGTTTATGGGATCAAAGCCTA      6420
```

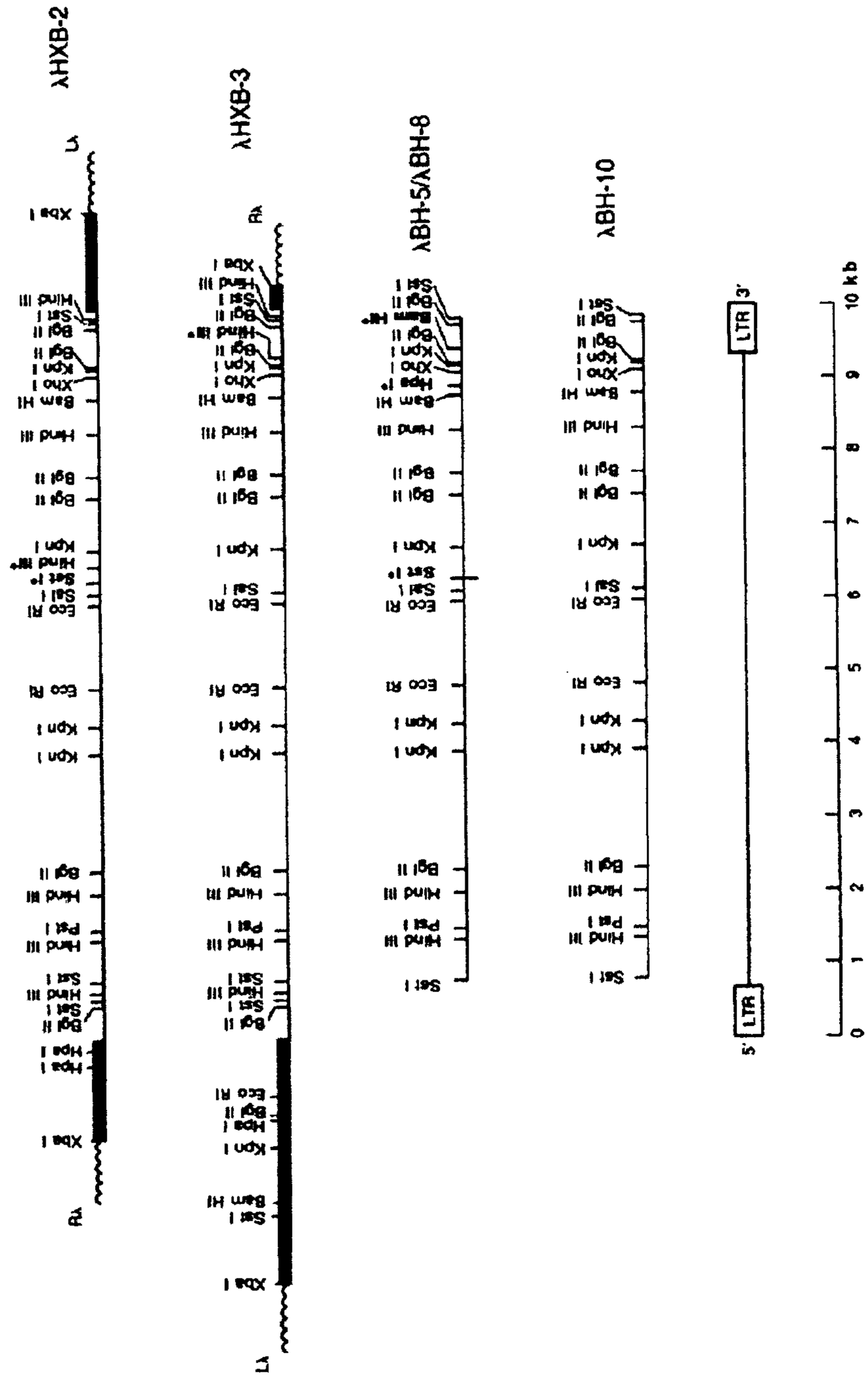
FIG. 7 (continued)

```
AAGCCATGTGTAAAATTAACCCCACTCTGTGTTAGTTTAAAGTGCACTGATTTGAAGAAT   6480
GATACTAATACCAATAGTAGTAGCGGGAGAATGATAATGGAGAAAGGAGAGATAAAAAAC   6540
TGCTCTTTCAATATCAGCACAAGCATAAGAGGTAAGGTGCAGAAAGAATATGCATTTTTT   6600
TATAAACTTGATATAATACCAATAGATAATGATACTACCAGCTATACGTTGACAAGTTGT   6660
AACACCTCAGTCATTACACAGGCCTGTCCAAAGGTATCCTTTGAGCCAATTCCCATACAT   6720
TATTGTGCCCCGGCTGGTTTTGCGATTCTAAAATGTAATAATAAGACGTTCAATGGAACA   6780
GGACCATGTACAAATGTCAGCACAGTACAATGTACACATGGAATTAGGCCAGTAGTATCA   6840
ACTCAACTGCTGTTAAATGGCAGTCTAGCAGAAGAAGAGGTAGTAATTAGATCTGCCAAT   6900
TTCACAGACAATGCTAAAACCATAATAGTACAGCTGAACCAATCTGTAGAAATTAATTGT   6960
ACAAGACCCAACAACAATACAAGAAAAAGTATCCGTATCCAGAGAGGACCAGGGAGAGCA   7020
TTTGTTACAATAGGAAAAATAGGAAATATGAGACAAGCACATTGTAACATTAGTAGAGCA   7080
AAATGGAATAACACTTTAAAACAGATAGATAGCAAATTAAGAGAACAATTTGGAAATAAT   7140
AAAACAATAATCTTTAAGCAGTCCTCAGGAGGGGACCCAGAAATTGTAACGCACAGTTTT   7200
AATTGTGGAGGGGAATTTTTCTACTGTAATTCAACACAACTGTTTAATAGTACTTGGTTT   7260
AATAGTACTTGGAGTACTAAAGGGTCAAATAACACTGAAGGAAGTGACACAATCACCCTC   7320
CCATGCAGAATAAAACAAATTATAAACATGTGGCAGGAAGTAGGAAAAGCAATGTATGCC   7380
CCTCCCATCAGTGGACAAATTAGATGTTCATCAAATATTACAGGGCTGCTATTAACAAGA   7440
GATGGTGGTAATAGCAACAATGAGTCCGAGATCTTCAGACCTGGAGGAGGAGATATGAGG   7500
GACAATTGGAGAAGTGAATTATATAAATATAAAGTAGTAAAAATTGAACCATTAGGAGTA   7560
GCACCCACCAAGGCAAAGAGAAGAGTGGTGCAGAGAGAAAAAAGAGCAGTGGGAATAGGA   7620
GCTTTGTTCCTTGGGTTCTTGGGAGCAGCAGGAAGCACTATGGGCGCAGCGTCAATGACG   7680
CTGACGGTACAGGCCAGACAATTATTGTCTGGTATAGTGCAGCAGCAGAACAATTTGCTG   7740
AGGGCTATTGAGGCGCAACAGCATCTGTTGCAACTCACAGTCTGGGGCATCAAGCAGCTC   7800
CAGGCAAGAATCCTGGCTGTGGAAAGATACCTAAAGGATCAACAGCTCCTGGGGATTTGG   7860
GGTTGCTCTGGAAAACTCATTTGCACCACTGCTGTGCCTTGGAATGCTAGTTGGAGTAAT   7920
AAATCTCTGGAACAGATTTGGAATAACATGACCTGGATGGAGTGGGACAGAGAAATTAAC   7980
AATTACACAAGCTTAATACACTCCTTAATTGAAGAATCGCAAAACCAGCAAGAAAAGAAT   8040
GAACAAGAATTATTGGAATTAGATAAATGGGCAAGTTTGTGGAATTGGTTTAACATAACA   8100
AATTGGCTGTGGTATATAAAATTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAGA   8160
ATAGTTTTTGCTGTACTTTCTGTAGTGAATAGAGTTAGGCAGGGATATTCACCATTATCG   8220
TTTCAGACCCACCTCCCAATCCCGAGGGGACCCGACAGGCCCGAAGGAATAGAAGAAGAA   8280
GGGGAGAGAGAGACAGAGACAGATCCATTCGATTAGTGAACGGATCCTTAGCACTTATCT   8340
GGGACGATCTGCGGAGCCTGTGCCTCTTCAGCTACCACCGCTTGAGAGACTTACTCTTGA   8400
TTGTAACGAGGATTGTGGAACTTCTGGGACGCAGGGGGTGGGAAGCCCTCAAATATTGGT   8460
GGAATCTCCTACAGTATTGGAGTCAGGAGCTAAAGAATAGTGCTGTTAGCTTGCTCAATG   8520
CCACAGCTATAGCAGTAGCTGAGGGGACAGATAGGGTTATAGAAGTAGTACAAGGAGCTT   8580
```

FIG. 7 (continued)

```
ATAGAGCTATTCGCCACATACCTAGAAGAATAAGACAGGGCTTGGAAAGGATTTTGCTAT      8640
AAGATGGGTGGCAAGTGGTCAAAAAGTAGTGTGGTTGGATGGCCTGCTGTAAGGGAAAGA      8700
ATGAGACGAGCTGAGCCAGCAGCAGATGGGGTGGGAGCAGCATCTCGAGACCTAGAAAAA      8760
CATGGAGCAATCACAAGTAGCAACACAGCAGCTAACAATGCTGATTGTGCCTGGCTAGAA      8820
GCACAAGAGGAGGAGGAGGTGGGTTTTCCAGTCACACCTCAGGTACCTTTAAGACCAATG      8880
ACTTACAAGGCAGCTGTAGATCTTAGCCACTTTTTAAAAGAAAAGGGGGGACTGGAAGGG      8940
CTAATTCACTCCCAACGAAGACAAGATATCCTTGATCTGTGGATCTACCACACACAAGGC      9000
TACTTCCCTGATTAGCAGAACTACACACCAGGGCCAGGGATCAGATATCCACTGACCTTT      9060
GGATGGTGCTACAAGCTAGTACCAGTTGAGCCAGAGAAGTTAGAAGAAGCCAACAAAGGA      9120
GAGAACACCAGCTTGTTACACCCTGTGAGCCTGCATGGAATGGATGACCCGGAGAGAGAA      9180
GTGTTAGAGTGGAGGTTTGACAGCCGCCTAGCATTTCATCACATGGCCCGAGAGCTGCAT      9240
CCGGAGTACTTCAAGAACTGCTGACATCGAGCTTGCTACAAGGGACTTTCCGCTGGGGAC      9300
TTTCCAGGAGGCGTGGCCTGGGCGGGACTGGGGAGTGGCGAGCCCTCAGATCCTGCATAT      9360
AAGGAGCTGCTTTTTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTGGGAG      9420
CTC
```

FIG. 7 (continued)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λHXB-3
λBH-5/λBH-8
λBH-10
LTR
3'
5'
10 kb
Xba I
Hind III
Sst I
Bgl II
Kpn I
Xho I
Bam HI
Eco RI
Sal I
Not I*
Pst I
Hpa I*

FIG. 8

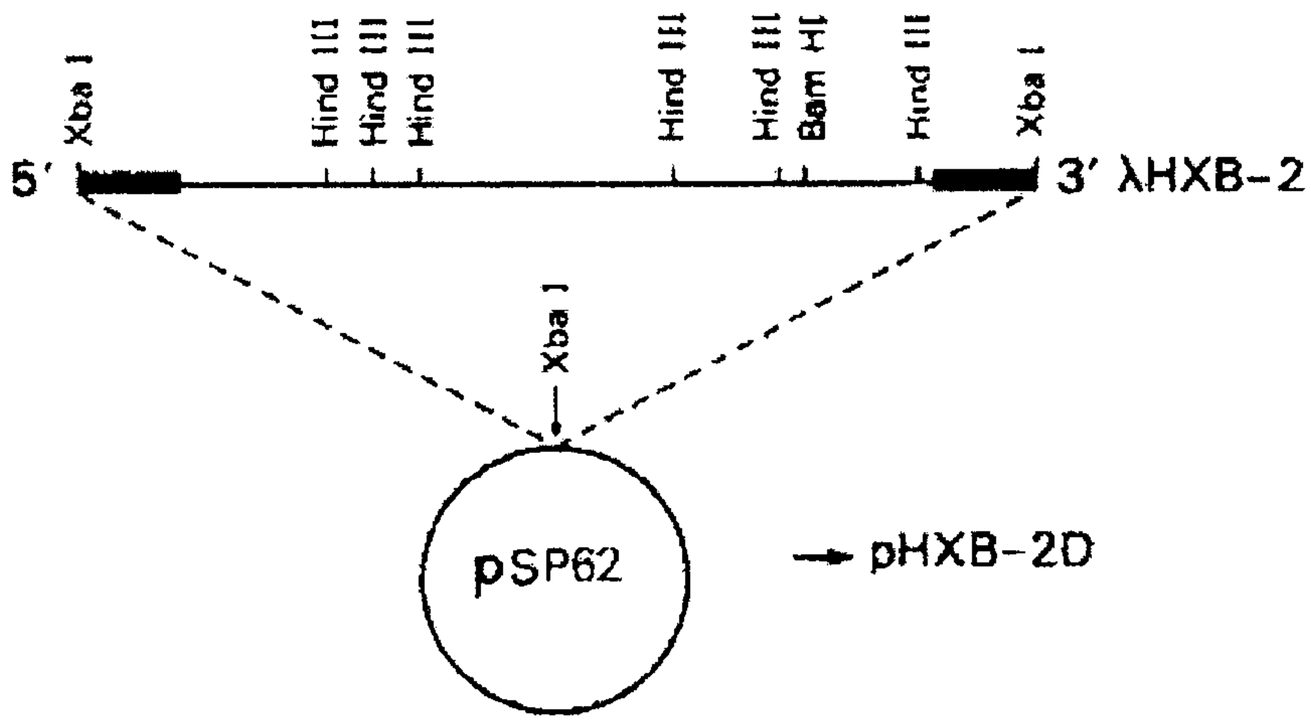
Xba I
Hind III
Hind III
Hind III
Hind III
Hind III
Bam HI
Hind III
Xba I
5'
3' λHXB-2
Xba I
pSP62
pHXB-2D

FIG. 9

MOLECULAR CLONING OF HIV-1 FROM IMMORTALIZED CELL LINES

REFERENCE TO RELATED APPLICATIONS

This application, Ser. No. 08/385,231, filed Feb. 8, 1995, is a file wrapper continuation of patent application Ser. No. 07/832,603, filed Feb. 12, 1992, now abandoned, which is a file wrapper continuation of patent application Ser. No. 07/160,827, filed Feb. 26, 1988, now abandoned, which is (i) a continuation-in-part of patent application Ser. No. 07/033,891, filed Apr. 3, 1987, now abandoned, which is a continuation of patent application Ser. No. 06/643,306, filed Aug. 22, 1984, now abandoned, (ii) a continuation-in-part of patent application Ser. No. 06/693,866, filed Jan. 23, 1985, pending, which is a continuation-in-part of patent application Ser. No. 06/659,339, filed Oct. 10, 1984, now abandoned, which is a continuation-in-part of patent application Ser. No. 06/643,306, filed Aug. 22, 1984, now abandoned, and (iii) a continuation-in-part of patent application Ser. No. 06/813,069, filed Dec. 24, 1985, now abandoned, the disclosures of which are incorporated herein by reference in their entirety for all purposes.

TERMINOLOGY

The causative agent of acquired immune deficiency syndrome (AIDS) has been known as human T-lymphotropic virus type III (HTLV-III) and as human immunodeficiency virus (HIV). The virus, in accord with the newer practice, will be called HIV except in some instances where a deposit relating to the organism has been made using the earlier terminology.

BRIEF DESCRIPTION OF THE INVENTION

The cultivation of viruses using molecular clones provides a dependable source of virus for study of the natural virus and for preparation of diagnostic and immunogenic products of the virus. The isolation of virus believed to be the causative agent of AIDS was reported by Barre-Sinoussi, et al. in *Science*, Vol. 220, at pages 868-870 (1983). However, no reproduction of the virus in an immortalized cell line is disclosed in that publication. HIV is highly cytopathic to the cells which it infects in nature. This is one characteristic which differentiates HIV from related retroviruses such as HTLV-I and HTLV-II. HIV is further characterized by variation of its genome in nature. Gallo, et al. discovered cell lines useful for continuous production of the virus. The use of such cell lines which are CD-4 positive cells was disclosed in U.S. patent application Ser. No. 06/652,599, which issued as U.S. Pat. No. 4,652,599. The disclosure of that patent is incorporated herein by reference. The disclosure herein provides means for producing clones of virus which are grown in the immortalized cell lines.

The infectious clones of the inventions are useful for producing specific viral proteins in both eukaryotic and prokaryotic systems for use in diagnostic evaluation and for vaccine development. The infectious clones also provide a source of homogeneous viral particles for use in evaluation of vaccines.

While HXB2 and HXB3 were shown to be non-infectious or only mildly infectious, infectious clones which have been derived therefrom are disclosed. Transfection of the derivative clones into bacteria provides a means for amplifications of the genome of these clones.

It is the object of this invention to provide a reliable source of HIV, viral particles, proteins, and antibodies by preparation of clones containing essentially the entire genome of the HIV. The virus or viral fragments produced in immortalized cell lines are useful as probes to detect HIV viral sequences in HIV strains isolated from patients. By use of such probes the variant strains of HIV can be studied as a means of determining source of the disease in an individual. Such determination of source is vital in evaluating means of transmission of this disease.

It is a further object of the invention to provide reliable sources of viral products for use as immunogens and diagnostic agents.

BACKGROUND OF THE INVENTION

The characterization of HIV as the causative agent of AIDS by Barre-Sinoussi, et al. [*Science*, Vol. 220 (1983)] did not provide enablement for producing the virus in vitro. However, it was discovered by workers in this laboratory that the causative agent of AIDS could be grown in immortalized CD-4 positive cell lines to provide a reliable source of the virus and viral products. The use of these products as diagnostic tools is disclosed in U.S. Pat. No. 4,520,113, which is incorporated herein by reference.

A method of cloning human T-cell leukemia-lymphoma virus (HTLV), a transforming virus which lacks both the variability and cytopathic properties of HIV, is taught in Manzari, et al., [Proc. Natl. Acad. Sci., Vol. 80, pages 1574-1577 (1983)]. There is no teaching of how to clone a highly cytopathic virus of such diverse genomic structure as the HIV. To obtain a virus for cloning, it was necessary to have an infected, immortalized cell line from which to extract the virus. U.S. Pat. No. 4,652,599 to Gallo, et al. teaches such cell lines.

DESCRIPTION OF THE FIGURES

FIG. **1** is a Southern blot analysis of unintegrated DNA of HIV. No viral sequences could be detected in the undigested DNA after 4 hours. However, a major species of viral DNA of approximately 10 kb length was present in the 10, 15, 24 and 48 hour harvest representing the linear unintegrated form of the virus. A representative Southern blot of the 15 hour harvest digested with several restriction enzymes is shown in this figure. Methods: 8×10^8 fresh uninfected H9 cells were infected with concentrated supernatant from cell line H9/HTLV-III (H9/HIV) containing 4×10^{11} particles of HIV. Infected cells were divided into five Roller bottles and harvested after 4, 10, 15, 24 and 48 hours. Low molecular weight DNA was prepared using the Hirt fractionation procedure and 30 g of undigested and digested DNA were separated on a 0.8% agarose gel, transferred to nitrocellulose paper and hybridized to a HIV cDNA probe for 24 hours at 37° C. in 1×SSC, 40% formamide and 10% Dextran sulfate. cDNA was synthesized from poly(A) selected RNA prepared from doubly banded HIV virus in the presence of oligo(dT) primers. Filters were washed at 1×SSC at 65° C.

FIG. **2** is a restriction endonuclease map of two closely related HIV variants cloned from unintegrated viral DNA. Three recombinant clones (λBH10, λBH5 and λBH8) were analyzed and their inserts (9 Kb, 5.5 Kb and 3.5 Kb, respectively) were mapped with the indicated enzymes. They represent two variant forms of HIV differing in three enzyme sites which are depicted in bold letters and by an asterisk. As SstI cuts the LTR of the HIV the three clones represent two full-length genomes with one LTR. A schematic map of this viral genome is shown at the bottom of the figure, although the total length of the LTR is approximate.

FIG. **3** demonstrates HIV viral sequences in the infected cell line H9/HIV. Both variant forms of HIV were detected as integrated provirus as well as unintegrated viral DNA in the infected cell line. However, no viral sequences were found in uninfected H9 cells, uninfected HT cells nor in normal human thymus (NT).

FIG. **4** shows a sequence homology of HIV to related retroviral members of the HTLV family. A schematic restriction map of HTLV-I, HTLV-Ib and HTLV-II is drawn below indicating the length and the location of the generated fragments in respect to the corresponding genomic regions.

FIG. **5** represents the entire nucleotide sequence of the molecular clone BH5 (ATCC #40126), which is approximately one half of a cloned genomic sequence for an HIV strain on deposit with the American Type Culture Collection.

FIG. **6** represents the entire nucleotide sequence of the molecular clone BH8 (ATCC #40127), which is approximately the second half of the genomic sequence for the HIV strain noted in FIG. **5**.

FIG. **7** represents the entire nucleotide sequence of the molecular clone BH10 (ATCC #40125), which is approximately the entire cloned genomic sequence of an HIV strain, different from the strain noted in FIGS. **5** and **6**, on deposit with the American Type Culture Collection.

FIG. **8** shows restriction endonuclease maps of four closely related clones of HIV. λHXB-2 and λHXB-3 represent full-length integrated proviral forms of HIV obtained from the λ phage library of H9/HIV DNA (Example 3). These clones contain the complete provirus (thin lines) including two LTR regions plus flanking cellular sequences (heavy lines). The LTR regions are known to contain the three restriction enzyme sites Bgl II, Sst I, and Hind III, as shown, but their overall lengths are estimated. Clones λBH-10 and λBH-5/λBH-8 are shown here for comparison with λHXB-2 and λHXB-3 and with Southern blots of genomic DNA from other HTLV-III containing cells. It should be noted that λBH-5/λBH-8 consists of two separate clones Sst I fragments (λBH-5 and λBH-8) which together constitute one HIV genomic equivalent but which are not necessarily derived from the same viral molecule. Also, because λBH-10 and λBH-5 were cloned with the restriction enzyme Sst I, they lack 5' LTR sequences as shown. Other differences in the restriction maps between these HIV clones are indicated by bold letters and asterisks, with λBH-10 being used as a reference.

FIG. **9** shows the construction of a plasmid containing sequences of the HIV genome. A 12.7-kb XbaI fragment derived from HXB-2, a molecular clone containing about 10 kb of HIV proviral sequences, was inserted into the XbaI site in the polylinker of plasmid pSP62 to produce the plasmid clone pHXB-2D. This plasmid construct was then transfected into DH-1 bacteria and used in protoplast fusion experiments. The thin horizontal line represents HIV and the solid boxes represent flanking cellular sequences.

DETAILED DESCRIPTION OF THE INVENTION

Clones are prepared using both unintegrated DNA and integrated DNA proviral DNA. The clones of integrated DNA and unintegrated DNA are similar, but are distinguishable by differences in several restriction cleavage sites. From FIG. **8**, it is shown λBH-10 and λBH-5/λBH-8 are incomplete viral clones which lack a short SstI-SstI segment of approximately 190 base pairs in the 5' LTR-leader sequence as a consequence of use of Sst I in their cloning. The λHXB-2 and λHXB-3 clones contain full-length integrated provirus [~10 kilobases (kb)] with cellular flanking sequences.

Plasmids are constructed using λHXB-2 to produce pHXB-2D A 12.7 kb XbaI fragment derived from pHXB-2D was inserted into the XbaI site in the polylinker of plasmid pSP62 to provide a plasmid suitable for transfection into the DH-1 bacteria.

Preparation of Clones λBH10, λBH5, and λBH8

Example 1

Concentrated virus from the H9/HTLV-III cell line as used to infect fresh uninfected H9 cells at a multiplicity of 50 viral particles per cell and cultures were collected after 4, 10, 15, 24 and 48 hours. Extrachromosomal DNA was extracted according to the procedure of Hirt [Hirt, R., *J. Molec. Biol.* 26: 365-367 (1967)] and assayed for its content of unintegrated viral DNA using HIV cDNA as a probe. The synthesis of this cDNA was primed with oligo(dT) and reverse-transcribed from poly(A)-containing RNA of virions that had been banded twice on sucrose density gradients [Arya, et al., *Science* 225: 927-930 (1984)]. Unintegrated linear viral DNA was first detected after 10 h and was also present at the subsequent time points. (FIG. **1** shows a Southern blot of the 15-h sampling.) A band of ~10 kilobases (kb) in the undigested DNA represents the linear form of unintegrated HIV. No closed or nicked circular DNA could be detected at 10, 15 or 24 hours, but both forms were evident in small amounts at 48 hours (data not shown). The viral genome was not cleaved by XbaI, whereas SstI generated three predominant bands of 9, 5.5 and 3.5 kb (FIG. **1**). These bands represent the genomes of two forms of HIV, both cut by SstI in or near the long terminal repeat (LTR), and one having an additional SstI site in the middle of its genome. The other enzymes generate a more complex pattern of restriction fragments.

FIG. **2** shows the restriction map of three clones, designated λBH10, λBH5 and λBH8, which correspond in size to the three SstI fragments shown in FIG. **1**. Comparison of these maps suggests that λBH5 plus λBH8 constitute one HIV genome, and BH10 another. The two viral forms differ in 3 of 21 mapped enzymes sites, including the internal SstI site. As expected, the phage inserts of λBH5 and λBH8 hybridize in high-stringency conditions (T_m-25° C.) to λBH10 but not to each other, as analyzed by Southern blot hybridization and electron microscopic hetero-duplex analysis (data not shown). To determine the orientation of the three clones, we used as a probe a cDNA clone (C15) containing U3 and R sequences. C15 hybridized strongly to the 0.5 kb BglII fragment of λBH10 and λBH8, orienting this side 3'. Assuming that SstI cuts only once in the vicinity of the HIV LTR, the clones λBH10 and λBH5/λBH8 represent two complete genomic equivalents of the linear unintegrated form of HIV that vary in three restriction enzyme sites.

Methods: Low molecular weight DNA combined from the 15 and 24 hour harvest was fractionated on a 10-40% sucrose gradient. Aliquots of the fractions were electrophoresed on a 0.5% agarose gel, transferred to nitrocellulose paper and hybridized to HIV cDNA under conditions described in FIG. **1**. Fractions which contained the unintegrated linear HIV genome shown by hybridization were pooled, the DNA was subsequently digested with SstI and ligated to phosphatase treated SstI arms of λgtWes. λB. After in vitro packaging, recombinant phages were screened for viral sequences with HIV cDNA.

Example 2

The presence of two variant forms of HIV in the original cell line was demonstrated by hybridizing the radiolabelled

insert of λBH10 to a Southern blot of H9/HIV genomic DNA digested with several restriction enzymes (FIG. **3**); both forms were detected using SstI, which generated the expected three bands of 9, 5.5 and 3.5 kb. XbaI, which does not cut the provirus, generated a high-molecular weight smear representing polyclonal integration of the provirus, plus a band of ~10 kb. This 10-kb band was also detected in undigested H9/HIV DNA (not shown), indicating that it represents unintegrated viral DNA. The presence of unintegrated viral DNA also explains the 4- and 4.5-kb EcoRI fragments seen in both the Hirt and total cellular DNA preparations (FIGS. **1**, **3**). Both BglII and HindIII cut within the LTR and generate the expected internal bands. Several faint bands in addition to the expected internal bands generated by HindIII digestion, represent either defective proviruses or other variant forms of HIV present in low copy number.

Method: 10 μg of high molecular weight DNA were digested with restriction enzymes as indicated and hybridized to nick translated phage insert from BH10 under the same conditions as described in FIG. **1**.

For comparison, sub-clones of full length genomes of a prototype HTLV-I, HTLV-Ib, HTLV and GaLV (Seato strain) were digested with the following enzymes, PstI plus SstI (HTLV-I and HTLV-Ib), BamHI plus SmaI (HTLV-II) and Hind III plus SmaI plus XhoI (GaLV). Four replicate filters were prepared and hybridized for 36 hours under low stringency (8×SSC, 20% formamide, 10% Dextran sulfate at 37° C.) to nick translated insert of λBH10. Filters were then washed in 1×SSC at different temperatures, 22° C. (Tm−70° C.) filter 1, 37° C. (Tm−56° C.) filter 2, 50° C. (Tm−42° C.) filter 3 and 65° C. (Tm−28° C.).

FIG. **4** shows a sequence homology between HIV and other related retroviruses. Hybridization of HIV with the related HTLV family could be detected where no hybridization to GaLV was seen.

Preparation of Clones Containing Integrated Proviral DNA

Example 3

The HIV is used to infect H9 cells in accord with the method of Example 1. Preliminary analyses of Southern digests of H9/HIV DNA reveals that the virus is present in this cell line both as unintegrated DNA and as proviral DNA integrated into the cellular genome at multiple different sites. Since the HIV provirus lacks Xba I restriction sites, a genomic library was constructed by using Xba I-digested H9/HIV DNA, and this was screened with an HIV cDNA probe to obtain molecular clones of full-length integrated provirus with flanking cellular sequences. Fourteen such clones were obtained from an enriched library of 10^6 recombinant phage, and two of these were plaque-purified and characterized. (See FIG. **8**.)

To show that the restriction enzyme cleavage sites depicted in FIG. **8** for clones λHXB-2 and λHXB-3 are actually present in the viral DNA of HIV-infected H9 cells, DNA was digested from the H9/HIV cell line with various restriction enzymes and analyzed it by the Southern blot technique. The restriction fragments for Sst I, Eco RI, Hind III, Pst I, Bam H1, and BglII predicted from the restriction maps of λHXB-2 and λHXB-3 (FIG. **8**) are shown to be present in the Southern blots of HIV infected cellular DNA.

Example 4

To determine whether the HIV genome contains sequences homologous to normal human DNA, the viral insert of λHXB-2 (5.5 kb and 3.5 kb Sst I-Sst I fragments) was isolated, nick translated, and used to probe HIV-infected and uninfected cellular DNA. Under standard conditions of hybridization [washing conditions: 1×SSC (standard saline citrate), 65° C.; annealing temperature T_m−27 C], this probe hybridizes to DNA from H9/HIV cells as well as other HIV-infected cells, but not to DNA from uninfected H9 cells, uninfected HT cells (the parent cell line from which H9 as cloned), or normal human tissues (data not shown). This finding is in agreement with previous results in which the unintegrated (replicative intermediate) form of HIV was used as probe and demonstrates that HIV, like HTLV-1 and HTLV-II, is an exogenous retrovirus lacking nucleic acid sequences derived from human DNA.

Example 5

A 12.7 kb XbaI fragment derived from λHXB-2 is inserted into the polylinker of plasmid pSP62 to produce plasmid clone pHXB-2D (FIG. **9**). The pHXB-2D is transfected into DH-1 bacteria for use in protoplast fusion experiments.

Example 6

Kinetics of cell growth and reverse transcriptase activity in cord blood mononuclear cell cultures following protoplast fusion: Mononuclear cells were prepared from cord blood samples using Ficoll Triosil and cultured for 5 days in media containing PHA. These cells were then fused with bacterial protoplasts carrying the plasmid pHXB-2D, pSV2neo or pCH-1gpt and maintained in culture at a density of 5×10^5 cells ml^{-1} by addition of RPMI-1640 medium containing 20% fetal calf serum, 10% T-cell growth factor (inter-leukin-2) and antibiotics. Three parallel fusions using cells from different individuals were established for each plasmid. Spent medium removed from two cultures at 5, 11, 14 and 18 days after fusion was concentrated 10-fold and assayed for the presence of reverse transcriptase using standard techniques. The activity detected in each of the culture supernatants is expressed as the amount of ^{3}H-labeled deoxyribonucleotide monophosphate (^{3}H-dTMP) incorporated (in pmol per 0.3-ml sample) using $dT_{15}\cdot(rA)_n$ as the template primer.

The growth of all cultures was comparable for the first 14 days after protoplast fusion. By day 18, however, the number of viable cells in cultures transfected with pHXB-2D had fallen dramatically: there was a 10-fold and a 100-fold reduction between days 18 and 21 and 18 and 32, respectively. Cultures transfected with either pSV2neo or pCH-1gpt showed only a 4-5-fold reduction over the same time period. When supernatant from the cultures was assayed for the presence of reverse transcriptase, activity was detected exclusively in cultures transfected with pHXB-2D. These data suggest that replicating virus was present in cultures 11-18 days after fusion with pHXB-2D protoplasts.

Example 7

Expression of the HIV gag-related proteins p15 and p24 by transfected cells was demonstrated using specific monoclonal antibodies. Maximum expression was observed 18 days after transfection, when 4-11% and 5-9% of cells were reactive with antibody to p15 and p24, respectively. Virus particles were detected by electron microscopy in all cultures 14-18 days after transfection with pHXB-2D. The particles contained condensed, truncated cores, which are characteristic of HIV particles.

Example 8

In time-course experiments, DNA isolated from a single culture 6, 11, 14, 18 and 31 days after transfection with pHXB-2D, was digested with BamHI and analyzed for HIV sequences. Six days after transfection, an 8.6-kb DNA fragment was detected as a faint band; 18 days after transfection it was possible to detect a 1.5-kb DNA fragment in addition to the 8.6-kb fragment. The total amount of unintegrated virus in the cultures appeared to increase, as suggested by the increase in intensity of these bands with time; this is evidence that cells originally transfected with pHXB-2D are able to produce fully infectious virus which is then transmitted within the culture.

No HIV viral sequences were detected 31 days after transfection; at this point the culture may have contained only cells which failed to be infected by HIV. This result is again consistent with the transfected DNA exerting a cytopathic effect on T cells. The finding that, at any stage, only a minor population of the transfected cells are apparently infected by the virus (<15% express viral proteins) suggests that the cytopathic effects may not result solely from direct viral infection and that secreted factors and/or other cell-to-cell interactions may play a part in the cytopathic phenomenon.

The biological materials relating to the invention have been deposited at the American Type Culture Collection, Rockville, Md., under the following accession numbers:

λBH-10	40125 (FIG. 7)
λBH-5	40126 (FIG. 5)
λBH-8	40127 (FIG. 6)
λ-HXB$_2$	40231
λ-HXB$_3$	40232
pHXB3	67081
pHXB-2D	67082
X10-1 (*E coli* DH-1)	67083

Upon issuance of a patent on the present invention, this deposit will continue to be viably maintained for 30 years and made available to the public without restriction, of course, consistent with the provisions of the law.

Examples of useful products are now described:

1. Viral particles and proteins may be extracted from both supernatants and whole cells.
2. Supernatant material may be purified for use in test kits for immunoblotting and immunoadsorbent tests.
3. Monoclonal antibodies may be produced which react against HIV antigens.
4. The antigens may be used as immunogens in vaccine development.

Both antibodies and antigens can be used in diagnostic kits. Both antibodies and antigens can be provided as compositions. Particularly preferred compositions of matter are solid supports having antigens of the invention adhering thereto for use in identifying antibodies to HIV proteins for use in Enzyme-linked-immunoabsorbent (ELISA) assays.

It is understood that the examples and embodiments described herein are for illustration purposes. Examples are not intended to be viewed as limitations since many obvious modifications are within the scope of one skilled in the art.

TABLE I

CLAIMS SUPPORT CHART

Claim	Support in U.S. patent application 06/643,306 filed on Aug. 22, 1984
61. (new) A method for detecting the presence of a polynucleotide comprising a human immunodeficiency virus (HIV) nucleotide sequence in a nucleic acid sample obtained from a physiological sample, which method comprises the steps of: (a) combining said nucleic acid sample with a single-stranded nucleic acid probe comprising a sequence of at least about 18 contiguous bases selected from one of the nucleotide sequences shown in FIGS. 5, 6 or 7 and complementary to said HIV genomic sequence comprised in said polynucleotide, said probe not forming a duplex with HTLV-I and -II nucleic acid sequences under conditions of stringency for hybridization under which said probe forms a duplex with said polynucleotide; and (b) determining duplex formation between said probe and nucleic acid present in said sample.	page 1, lines 28-34. discusses the use of cDNA clones of the invention to distinguish HTLV III from HTLV I and II. p. 3 line 25 to p. 4 line 8 discuss regions of homology and regions of variability between HTLV III, and HTLV I and II, that can be exploited in distinguishing between the different viruses. p. 5, lines 12-14 discusses production of a cDNA library for use in analyzing the HIV genome. p. 5 line 29 - p. 6 line 10 provides support for making probes from HIV mRNA. p. 6, lines 23-26 discusses using probes to assay viral DNA p. 7, lines 18-30 discuss using an λ phage clone in Southern analysis of restriction fragments from HIV DNA. Statement of Deposit, p. 6. p. 1 discussion relating to detection of HIV in human sera. BH10 contains an 18 base BglII-SstI restriction fragment. FIG. 4 shows that only a fraction of the HTLV-I and -II genomes hybridize to HTLV-III. Example 2, p. 8 discusses the use of stringency washes to distinguish homology between HIV, HTLV I and HTLV II.
62. (new) The method of claim 61 wherein the probe sequence is complementary to a sequence which is part of the gag, pol or env open reading frame. 63. (new) The method of claim 62 wherein the probe sequence is complementary to a sequence which is part of the gag open reading frame. 64. (new) The method of claim 62 wherein the probe is complementary to a sequence which is part of the pol open reading frame.	p. 3 contains a discussion relating to the presence of gag, pol and env in HTLV-III.
65. (new) The method of claim 61 wherein the probe comprises RNA. 67. (new) The method of claim 62 wherein the probe comprises RNA.	p. 5 discussion of the use of RNA as probe/probe template.
66. (new) The method of claim 61 wherein the probe comprises DNA. 68. (new) The method of claim 62 wherein the probe comprises DNA.	Support noted for claim 1 refers to DNA probes

TABLE I-continued

CLAIMS SUPPORT CHART

Claim	Support in U.S. patent application 06/643,306 filed on Aug. 22, 1984
69. (new) A method comprising the steps of: (a) providing a sample suspected of containing a polynucleotide; (b) providing a single-stranded nucleic acid of 18-103 bases comprising a sequence of bases of at least 18 contiguous bases selected from the gag, env, or pol open reading frames of FIG. 5, 6 or 7 or the complement thereof; and (c) combining said sample and said single-stranded nucleic acid under hybridization conditions that (i) permit duplex formation between said single-stranded nucleic acid and either strand of viral DNA from a lambda bacteriophage selected from the group consisting of ATCC Accession no. 40143 and 40144, but (ii) do not permit duplex formation with either HTLV-I or HTLV-II genomic sequences.	Support noted for claim 61 also applies here. clone BH5 contains a HindIII-XbaI fragment that is 103 bases in length. p. 3 contains a discussion relating to the presence of gag, pol and env in HTLV-III.
70. (new) A method comprising the steps of: (a) providing a sample suspected of containing a polynucleotide; (b) providing a single-stranded nucleic acid of 32-103 bases comprising a sequence of bases of at least 32 contiguous bases selected from the gag, env, or pol open reading frames of FIG. 5, 6 or 7 or the complement thereof; and (c) combining said sample and said single-stranded nucleic acid under hybridization conditions that (i) permit duplex formation between said single-stranded nucleic acid and either strand of viral DNA from a lambda bacteriophage selected from the group consisting of ATCC Accession no. 40143 and 40144, but (ii) do not permit duplex formation with either HTLV-I or HTLV-II genomic sequences.	
71. (new) The method of claim 69 or 70 wherein contiguous bases are from the gag open reading frame or the complement thereof.	p. 3 contains a discussion relating to the presence of gag, pol and env in HTLV-III.
72. (new) The method of claim 69 or 70 wherein said contiguous bases are from the env open reading frame or the complement thereof.	
73. (new) The method of claim 69 or 70 wherein said contiguous bases are from the pol open reading frame or the complement thereof.	
74. (new) The method of claim 61, 69 or 70 wherein said single-stranded nucleic acid comprises DNA and wherein said contiguous bases are within a restriction fragment produced by cleavage of the nucleic acid presented in FIG. 5, 6 or 7 using one or more restriction enzymes selected from the group consisting of SstI, HindIII, PstI, Bgl II, Kpn I, EcoRI, BamHI, HpaI, XhoI, XbaI and SmaI.	SstI pg. 2 and FIG. 2; HindIII pg. 4, and FIG. 2; PstI pg. 2 and FIG. 2 Bgl II pg. 7 and FIG. 2; Kpn I FIG. 2; EcoRI Page 7 and FIG. 2; BamHI Page 2 and FIG. 2; HpaI Page 2 and FIG. 2; XhoI Page 2 and FIG. 2; XbaI Page 7 and FIG. 3; and SmaI FIG. 2.
75. (new) The method of claim 74 wherein the single-stranded nucleic acid probe comprises one of the nucleotide sequences selected from the group consisting of: [Restriction Fragments supported in Wong-Staal specification.]	p. 9, lines 28-32 discusses the use of λBH10 and restriction fragments to analyze the HIV genome. p. 6, lines 23-26 discusses using cDNA to detect viral DNA
76. (new) The method of claim 75, wherein the single-stranded nucleic acid is 5'-CTTTAAGACCAATGACTTACAAGGCAGCTGTA -3'.	p. 7, lines 18-30 and p. 9 lines 15-26 discuss using an λ phage clone in Southern analysis of restriction fragments from HIV DNA. 32 nucleotide restriction fragment present in BH8. Nucleotide sequence of claim 76 nucleic acid is a 32 nucleotide KpnI-BglII restriction fragment from clone BH8
77. (new) A method for detecting the presence of a polynucleotide comprising a human immunodeficiency virus (HIV) nucleotide sequence in a nucleic acid sample obtained from a physiological sample, which method comprises the steps of: (a) combining said nucleic acid sample with a single-stranded nucleic acid probe comprising a sequence of at least about 32 contiguous bases selected from one of the nucleotide sequences shown in FIGS. 5, 6 or 7 and complementary to said HIV genomic sequence comprised in said polynucleotide, said probe not forming a duplex with HTLV-I and -II nucleic acid sequences under conditions of stringency for hybridization under which said probe forms a duplex with said polynucleotide; and (b) determining duplex formation between said probe and nucleic acid present in said sample.	Support cited for claim 1 is applicable here. See also support for claim 76.
78. (new) The method of claim 61, wherein the single-stranded nucleic acid probe is 5'- GATCTGAGCCTGGGAGCT-3'.	18 base BglII-SstI restriction fragment of BH10.
79. (new) The method of any of claims 69-73 wherein said single-stranded nucleic acid comprises RNA.	Discussion on p. 5 relating to the use of RNA as probe/probe template.
80. (new) The method of any of claims 69-73 wherein said single-stranded nucleic acid comprises DNA.	p. 1, lines 28-34. discusses the use of cDNA clones of the invention to distinguish HTLV III from HTLV I and II.
81. (new) The method of claim 79 wherein said single-stranded nucleic acid further comprises a label.	Original claim 5 discusses radiolabels. FIGS. 1, 3 and 4 show assays using labeled DNA.
82. (new) The method of claim 80 wherein said single-stranded nucleic acid further comprises a label.	p5, lines 24-26 discuss labeled probes, and p. 7 lines 18-22 discuss nick translation.
83. (new) The method of claims 69-73, wherein said sample is a human sample.	p. 1 contains a discussion of the use of probes to detect HTLV-III in human sera.

TABLE I-continued

CLAIMS SUPPORT CHART

Claim	Support in U.S. patent application 06/643,306 filed on Aug. 22, 1984
84. (new) The method of claim 83, wherein said human sample is blood, lymph or saliva.	
85. (new) The method of claims 84, wherein said sample is blood.	
86. (new) A method for detecting the presence of a polynucleotide comprising a human immunodeficiency virus (HIV) nucleotide sequence in a nucleic acid sample, the method comprising the steps of: (a) combining said nucleic acid sample with a single-stranded nucleic acid probe hybridizing under stringent conditions to an HIV nucleotide sequence present in a nucleic acid deposit selected from the group consisting of H9/HTLV-III cell line, CRL 8543; BH10, ATCC #40125; BH8, ATCC #40127; and BH5, ATCC #40126, said probe not forming a duplex with HTLV-I and -II nucleic acid sequences under conditions of stringency for hybridization that allow said probe to form a duplex with said polynucleotide; and (b) determining duplex formation between said probe and said nucleic acid present in said sample.	page 1, lines 28-34. discusses the use of cDNA clones of the invention to distinguish HTLV III from HTLV I and II. p. 3 line 25 to p. 4 line 8 discuss regions of homology and regions of variability between HTLV III, and HTLV I and II, that can be exploited in distinguishing between the different viruses. p. 5, lines 12-14 discusses production of a cDNA library for hybridization analysis of the HIV genome. p. 5 line 29 - p. 6 line 10 provides support for making cDNA probes from HIV mRNA. p. 6, lines 23-26 discusses using cDNA probes to assay viral DNA p. 7, lines 18-30 discuss using an λ phage clone in southern analysis of restriction fragments from HIV DNA by Southern blot. Statement of Deposit, p. 6. Example 2, p. 8 discusses the use of stringency washes to distinguish homology between HIV, HTLV I and HTLV II.
87. (new) The method of claim 86, wherein the nucleic acid probe is a restriction fragment.	p. 5 lines 23-28 discuss hybridizing cDNA sequences to genomic restriction fragments of HIV. p. 5, lines 12-14 discusses production of a cDNA library for hybridization analysis of the HIV genome.
88. (new) The method of claim 86, wherein the probe sequence is complementary to a sequence that is part of the gag, pol or env coding regions.	p. 5 lines 23-28 discuss hybridizing cDNA sequences to genomic restriction fragments of HIV. See also, FIG. 4 (restriction map) and p. 3, line 30 to p. 4 line 3.
89. (new) The method of claim 86, wherein the probe comprises DNA.	Support noted for claim 1 refers to DNA probes
90. (new) The method of claim 87, wherein the probe comprises DNA.	
91. (new) A method comprising the steps of: (a) providing a sample suspected of containing a polynucleotide; (b) providing a single-stranded HIV cDNA; and, (c) combining said sample and said single-stranded HIV cDNA under hybridization conditions that (i) permit duplex formation between said HIV cDNA and either nucleotide strand from a lambda bacteriophage selected from the group consisting of λBH10, λBH5 and λBH8, but (ii) do not permit duplex formation with either HTLV-I or HTLV-II genomic sequences.	p. 1, lines 28-34. discusses the use of cDNA clones of the invention to distinguish HTLV III from HTLV I and II. p. 3 line 25 to p. 4 line 8 discuss regions of homology and regions of variability between HTLV III, and HTLV I and II, that can be exploited in distinguishing between the different viruses. p. 5, lines 12-14 discusses production of a cDNA library for hybridization analysis of the HIV genome. p. 5 line 29 - p. 6 line 10 provides support for making cDNA probes from HIV mRNA. p. 9, lines 28-32 discusses the use of the λBH10 clone and HIV genomic restriction fragments in hybridization studies. p. 6, lines 23-26 discusses using cDNA probes to assay viral DNA p. 7, lines 18-30 and p. 9 lines 15-26 discuss using an λ phage clone in Southern analysis of restriction fragments from HIV DNA. Statement of Deposit, p. 6. Example 2, p. 8 discusses the use of stringency washes to distinguish homology between HIV, HTLV I and HTLV II.
92. (new) The method of claim 91, wherein said single-stranded nucleic acid is an SstI fragment or complement thereof.	FIGS. 2 and 3 provide restriction maps that would allow one of skill to identify probes to particular genomic regions. p. 9, lines 28-32 specifically discusses use probes to analyze restriction fragments. Also note discussion from p. 5, line 29 to p. 6, line 26 regarding the use of cDNA probes See also, FIG. 4 and p. 3, line 30 to p. 4 line 3.
93. (new) The method of claim 91 wherein said single-stranded nucleic acid is a HindIII fragment or complement thereof.	FIGS. 2 and 3 provide restriction maps that would allow one of skill to identify probes to particular genomic regions. p. 9, lines 28-32 specifically discusses hybridization analysis using restriction fragments. Also note discussion from p. 5, line 29 to p. 6, line 26 regarding the use of cDNA sequences as probes. See also, FIG. 4 and p. 3, line 30 to p. 4 line 3.
94. (new) The method of claim 91 wherein said single-stranded nucleic acid comprises DNA and hybridizes to a restriction fragment generated by treating an HIV genomic nucleic acid with HindIII and BamHI.	FIGS. 2 and 3 provide restriction maps that would allow one of skill to identify probes to particular genomic regions. p. 9, lines 28-32 specifically discusses use probes to analyze restriction fragments. Also note discussion from p. 5, line 29 to p. 6, line 26 regarding the use of cDNA probes See also, FIG. 4 and p. 3, line 30 to p. 4 line 3.
95. (new) The method of any of claims 91-94 wherein said single-stranded nucleic acid comprises DNA.	p. 1, lines 28-34. discusses the use of cDNA clones of the invention to distinguish HTLV III from HTLV I and II.
96. (new) The method of claim 95 wherein said single-stranded nucleic acid further comprises a label.	Original claim 5 discusses radiolabels. FIGS. 1, 3 and 4 show assays using labeled DNA. p5, lines 24-26 discuss labeled probes, and p. 7 lines 18-22 discuss nick translation.
97. (new) The method of claim 92 wherein said single-stranded nucleic acid comprises DNA and wherein said contiguous bases are within the gag open reading frame.	FIGS. 2 and 3 provide restriction maps that would allow one of skill to identify probes to particular genomic regions. p. 9, lines 28-32 specifically discusses hybridization analysis using restriction fragments. Also note discussion from p. 5, line 29 to p. 6, line 26 regarding the use of cDNA sequences as probes. See also, FIG. 4 and p. 3, line 30 to p. 4 line 3.

TABLE I-continued

CLAIMS SUPPORT CHART

Claim	Support in U.S. patent application 06/643,306 filed on Aug. 22, 1984
98. (new) The method of claim 97 wherein said single-stranded nucleic acid further comprises a label.	Original claim 5 discusses radiolabels. FIGS. 1, 3 and 4 show assays using labeled DNA. p5, lines 24-26 discuss labeled probes, and p. 7 lines 18-22 discuss nick translation.
99. (new) A method for detecting the presence of a polynucleotide comprising a human immunodeficiency virus (HIV) genomic sequence in a nucleic acid sample obtained from a physiological sample, which method comprises the steps of: (a) combining said nucleic acid sample with a single-stranded nucleic acid probe comprising a sequence of at least about 20 contiguous bases selected from the nucleotide sequences shown in FIGS. 5-7 and complementary to said HIV genomic sequence comprised in said polynucleotide, said probe not forming a duplex with HTLV-I and -II nucleic acid sequences under conditions of stringency for hybridization under which said probe forms a duplex with said polynucleotide; and (b) determining duplex formation between said probe and nucleic acid present in said sample.	page 1, lines 28-34. discusses the use of cDNA clones of the invention to distinguish HTLV III from HTLV I and II. p. 3 line 25 to p. 4 line 8 discuss regions of homology and regions of variability between HTLV III, and HTLV I and II, that can be exploited in distinguishing between the different viruses. p. 5, lines 12-14 discusses production of a cDNA library for use in hybridization studies of the HIV genome. p. 5 line 29 - p. 6 line 10 provides support for making cDNA probes from HIV mRNA. p. 6, lines 23-26 discusses using cDNA sequences for use in hybridization studies of the HIV genome. p. 7, lines 18-30 discuss using an λ phage clone in Southern analysis of restriction fragments from HIV DNA. Statement of Deposit, p. 6. p. 1 discussion relating to detection of HIV in human sera. BH10 contains an 18 base BglII-SstI restriction fragment. p. 3 contains a discussion relating to the presence of gag, pol and env in HTLV-III.
100. (new) The method of claim 99 wherein the probe sequence is complementary to a sequence which is part of the gag, pol or env open reading frame. 101. (new) The method of claim 100 wherein the probe sequence is complementary to a sequence which is part of the gag open reading frame. 102. (new) The method of claim 100 wherein the probe is complementary to a sequence which is part of the pol open reading frame.	
103. (new) The method of claim 99 wherein the probe comprises RNA. 105. (new) The method of claim 100 wherein the probe comprises RNA.	p. 5 discussion of the use of RNA as probe/probe template.
104. (new) The method of claim 99 wherein the probe comprises DNA. 106. (new) The method of claim 100 wherein the probe comprises DNA.	Support noted for claim 1 refers to DNA probes
107. (new) A method comprising the steps of: (a) providing a sample suspected of containing a polynucleotide; (b) providing a single-stranded nucleic acid of 20-100 bases comprising a sequence of bases of at least 20 contiguous bases selected from the gag, env, or pol open reading frames; and (c) combining said sample and said single-stranded nucleic acid under hybridization conditions that (i) permit duplex formation between said single-stranded nucleic acid and either strand of viral DNA from a lambda bacteriophage selected from the group consisting of ATCC Accession no. 40143 and 40144, but (ii) do not permit duplex formation with either HTLV-I or HTLV-II genomic sequences.	Support noted for claim 61 also applies here. p. 3 contains a discussion relating to the presence of gag, pol and env in HTLV-III.
108. (new) The method of any of claims 107 wherein said single-stranded nucleic acid comprises RNA.	p. 5 discussion of the use of RNA as probe/probe template.
109. (new) The method of any of claims 107 wherein said single-stranded nucleic acid comprises DNA.	Support noted for claim 1 refers to DNA probes
110. (new) The method of claim 108 wherein said single-stranded nucleic acid further comprises a label.	Original claim 5 discusses radiolabels. FIGS. 1, 3 and 4 show assays using labeled DNA.
111. (new) The method of claim 109 wherein said single-stranded nucleic acid further comprises a label.	p5, lines 24-26 discuss labeled probes, and p. 7 lines 18-22 discuss nick translation.
112. (new) The method of claim 108 wherein said single-stranded nucleic acid is chemically synthesized at least in part.	The paragraph spanning pages 5 and 6 discusses chemically synthesizing DNA using NaOH, an RNA template, and restriction enzymes.
113. (new) The method of claim 109 wherein said single-stranded nucleic acid is chemically synthesized at least in part. 114. (new) The method of claim 110 wherein said single-stranded nucleic acid is chemically synthesized at least in part. 115. (new) The method of claim 111 wherein said single-stranded nucleic acid is chemically synthesized at least in part.	
116. (new) The method of claims 99 or 101 wherein said sample is a human sample.	p. 1 contains a discussion of the use of probes to detect HTLV-III in human sera.
117. (new) The method of claim 116 wherein said human sample is blood, lymph or saliva. 118. (new) The method of claims 99 or 101 wherein said sample is blood, lymph or saliva.	

TABLE II

(BH 5 and 8 v. LUCIW)
89.8% identity

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                10        20        30        40        50
BH 8    -TGGAAGGGCTAATTCACTCCCAACGAAGACAAGATATCCTTGATCTGTGGATCCACCAC
         :::::::::::::    :::::: :::::::::: :::::::::::::::::: :::::
Licuw, CTGGAAGGGCTAATTTGGTCCCAAAGAAGACAAGAGATCCTTGATCTGTGGATCTACCAC
               10        20        30        40        50        60

      60        70        80        90       100       110
BH 8    ACACAAGGCTACTTCCCTGATTGGCAGAACTACACACCAGGGCCAGGAGTCAGATATCCA
        :::::::::::::::::::::::::::: ::::::::::::::::  ::::::::::
Licuw, ACACAAGGCTACTTCCCTGATTGGCAGAATTACACACCAGGGCCAGGGATCAGATATCCA
               70        80        90       100       110       120

     120       130       140       150       160       170
BH 8    CTGACCTTTGGATGGTGCTACAAGCTAGTACCAGTTGAGCCAGAGAAGTAAGAAGAAGCC
        :::::::::::::::::: :::::::::::::::::::::::::::  :::::: :::
Licuw, CTGACCTTTGGATGGTGCTTCAAGCTAGTACCAGTTGAGCCAGAGAAGGTAGAAGAGGCC
              130       140       150       160       170       180

     180       190       200       210       220       230
BH 8    AATAAAGGAGAGAACACCAGCTTGTTACACCCTGTGAGCCTGCATGGAATTGATGACCCG
        ::: :::::::::::: ::::::::::::::: :::::::::::: :: :: ::: ::
Licuw, AATGAAGGAGAGAACAACAGCTTGTTACACCCTATGAGCCTGCATGGGATGGAGGACGCG
              190       200       210       220       230       240

     240       250       260       270       280       290
BH 8    GAGAGAGAAGTGTTAGAGTGGAGGTTTGACAGCCGCCTAGCATTTCATCACATGGCCCGA
        :::: :::::::::: ::::::::::::::   ::::::::::::::::::::::::
Licuw, GAGAAAGAAGTGTTAGTGTGGAGGTTTGACAGCAAACTAGCATTTCATCACATGGCCCGA
              250       260       270       280       290       300

     300       310       320       330       340       350
BH 8    GAGCTGCATCCGGAGTACTTCAAGAACTGCTGACATCGAGCTTGCTACAAGGGACTTTCC
        :::::::::::::::::: :::  :::::::::::::::: ::::::::::::::::
Licuw, GAGCTGCATCCGGAGTACTACAAAGACTGCTGACATCGAGCTTTCTACAAGGGACTTTCC
              310       320       330       340       350       360

     360       370       380       390       400       410
BH 8    GCTGGGGACTTTCCAGGGAGGCGTGGCCTGGGCGGGACTGGGGAGTGGCGAGCCCTCAGA
        :::::::::::::::::::::::::::::::::::::::::::::::::  ::::::::
Licuw, GCTGGGGACTTTCCAGGGAGGCGTGGCCTGGGCGGGACTGGGGAGTGGCGT-CCCTCAGA
              370       380       390       400       410

     420       430        440       450       460       470
BH 8    TCCTGCATATAAGCAG-CTGCTTTTTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATCT
        : :::::::::::::: ::::::::::::::::::::::::::::::::::::::::::
Licuw, TGCTGCATATAAGCAGACTGCTTTTTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATCT
     420       430       440       450       460       470

      480       490
BH 8    GAGCCTGGGAGCTC----------------------------------------------
        ::::::::::::::
Licuw, GAGCCTGGGAGCTCTCTGGCTAACTAGGGAACCCACTGCTTAAGCCTCAATAAAGCTTGC
     480       490       500       510       520       530

-------------------------------------------------------------------

Licuw, CTTGAGTGCTTCAAGTAGTGTGTGCCCGTCTGTTGTGTGACTCTGGTAACTAGAGATCCC
     540       550       560       570       580       590

-------------------------------------------------------------------

Licuw, TCAGACCCTTTTAGTCAGTGTGGAAAAATCTCTAGCAGTGGCGCCCGAACAGGGACGCGA
     600       610       620       630       640       650

                                500       510       520       530
BH 5    --------------------GAGCTCTCTCGACGCAGGACTCGGCTTGCTGAAGCGCGCA
                            :::::::::::::::::::::::::::::::::::::::
Licuw, AAGCGAAAGTAGAACCAGAGGAGCTCTCTCGACGCAGGACTCGGCTTGCTGAAGCGCGCA
     660       670       680       690       700       710

            540       550       560       570       580       590
BH 5    CGGCAAGAGGCGAGGGGCGGCGACTGGTGAGTACGCCAAAAATTTTGACTAGCGGAGGCT
        : ::::::::::::::::::::::::::::::::::   :::::::::::::::::
Licuw, CAGCAAGAGGCGAGGGGCGGCGACTGGTGAGTACGCCAAT--TTTTGACTAGCGGAGGCT
     720       730       740       750         760       770

            600         610       620       630       640       650
```

TABLE II-continued

(BH 5 and 8 v. LUCIW)
89.8% identity

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BH 5    AGAAGGAGAGAGA--TGGGTGCGAGAGCGTCAGTATTAAGCGGGGGAGAATTAGATCGAT
        :::::::::::::  ::::::::::::::::: ::::::::::::::::::::::::  ::
Licuw,  AGAAGGAGAGAGAGATGGGTGCGAGAGCGTCGGTATTAAGCGGGGGAGAATTAGATAAAT
        780        790        800        810        820        830

                660        670        680        690        700        710
BH 5    GGGAAAAAATTCGGTTAAGGCCAGGGGGAAAGAAAAAATATAAATTAAAACATATAGTAT
        ::::::::::::::::::::::::::::::::::::::::::::: ::::::::::::::::
Licuw,  GGGAAAAAATTCGGTTAAGGCCAGGGGGAAAGAAAAAATATAAGTTAAAACATATAGTAT
        840        850        860        870        880        890

                720        730        740        750        760        770
BH 5    GGGCAAGCAGGGAGCTAGAACGATTCGCAGTTAATCCTGGCCTGTTAGAAACATCAGAAG
        :::::::::::::::::::::::::::::: :::::::::::::::::::::::::::::
Licuw,  GGGCAAGCAGGGAGCTAGAACGATTCGCAGTCAATCCTGGCCTGTTAGAAACATCAGAAG
        900        910        920        930        940        950

                780        790        800        810        820        830
BH 5    GCTGTAGACAAATACTGGGACAGCTACAACCATCCCTTCAGACAGGATCAGAAGAACTTA
        :::: ::::::::: :::::::::::::: ::::::::::::::::::::::::::::::
Licuw,  GCTGCAGACAAATATTGGGACAGCTACAGCCATCCCTTCAGACAGGATCAGAAGAACTTA
        960        970        980        990       1000       1010

                840        850        860        870        880        890
BH 5    GATCATTATATAATACAGTAGCAACCCTCTATTGTGTGCATCAAAGGATAGAGATAAAAG
        :::::::::::::::::::::::::::::::::::: :::::::::::::  ::::::
Licuw,  GATCATTATATAATACAGTAGCAACCCTCTATTGTGTACATCAAAGGATAGATGTAAAAG
       1020       1030       1040       1050       1060       1070

                900        910        920        930        940        950
BH 5    ACACCAAGGAAGCTTTAGACAAGATAGAGGAAGAGCAAAACAAAAGTAAGAAAAAAGCAC
        :::::::::::::::::::: :::::::::::::::::::::::::::::::::::: ::::
Licuw,  ACACCAAGGAAGCTTTAGAGAAGATAGAGGAAGAGCAAAACAAAAGTAAGAAAAAGGCAC
       1080       1090       1100       1110       1120       1130

                960                970        980        990       1000
BH 5    AGCAAGCAGCAGCTGA------CACAGGACACAGCAGTCAGGTCAGCCAAAATTACCCTA
        ::::::::::::::       :::::::::::::::: :::::::::::::::::::::
Licuw,  AGCAAGCAGCAGCTGCAGCTGGCACAGGAAACAGCAGCCAGGTCAGCCAAAATTACCCTA
       1140       1150       1160       1170       1180       1190

          1010       1020       1030       1040       1050       1060
BH 5    TAGTGCAGAACATCCAGGGGCAAATGGTACATCAGGCCATATCACCTAGAACTTTAAATG
        :::::::::::: : ::::::::::::::::::::::::::::::::::::::::::::::
Licuw,  TAGTGCAGAACCTACAGGGGCAAATGGTACATCAGGCCATATCACCTAGAACTTTAAATG
       1200       1210       1220       1230       1240       1250

          1070       1080       1090       1100       1110       1120
BH 5    CATGGGTAAAAGTAGTAGAAGAGAAGGCTTTCAGCCCAGAAGTAATACCCATGTTTTCAG
        :::::::::::::::::::: ::::::::::::::::::::::::::::::::::::::
Licuw,  CATGGGTAAAAGTAGTAGAAGAAAAGGCTTTCAGCCCAGAAGTAATACCCATGTTTTCAG
       1260       1270       1280       1290       1300       1310

          1130       1140       1150       1160       1170       1180
BH 5    CATTATCAGAAGGAGCCACCCCACAAGATTTAAACACCATGCTAAACACAGTGGGGGGAC
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Licuw,  CATTATCAGAAGGAGCCACCCCACAAGATTTAAACACCATGCTAAACACAGTGGGGGGAC
       1320       1330       1340       1350       1360       1370

          1190       1200       1210       1220       1230       1240
BH 5    ATCAAGCAGCCATGCAAATGTTAAAAGAGACCATCAATGAGGAAGCTGCAGAATGGGATA
        :::::::::::::::::::::::::::::: :::::::::::::::::::::::::::::
Licuw,  ATCAAGCAGCCATGCAAATGTTAAAAGAGACTATCAATGAGGAAGCTGCAGAATGGGATA
       1380       1390       1400       1410       1420       1430

          1250       1260       1270       1280       1290       1300
BH 5    GAGTGCATCCAGTGCATGCAGGGCCTATCGCACCAGGCCAGATGAGAGAACCAAGGGGAA
        :::::::::::::::::::::::::::: :::::::::: :::::::::::::::::::
Licuw,  GAGTGCATCCAGTGCATGCAGGGCCTATTGCACCAGGCCAAATGAGAGAACCAAGGGGAA
       1440       1450       1460       1470       1480       1490

          1310       1320       1330       1340       1350       1360
BH 5    GTGACATAGCAGGAACTACTAGTACCCTTCAGGAACAAATAGGATGGATGACAAATAATC
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Licuw,  GTGACATAGCAGGAACTACTAGTACCCTTCAGGAACAAATAGGATGGATGACAAATAATC
       1500       1510       1520       1530       1540       1550
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TABLE II-continued

(BH 5 and 8 v. LUCIW)
89.8% identity

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         1370      1380      1390      1400      1410      1420
BH 5   CACCTATCCCAGTAGGAGAAATTTATAAAAGATGGATAATCCTGGGATTAAATAAAATAG
       :::::::::::::::::::: :::::::::::::::::::::::::::::::::::::
Licuw, CACCTATCCCAGTAGGAGAAATCTATAAAAGATGGATAATCCTGGGATTAAATAAAATAG
      1560      1570      1580      1590      1600      1610

         1430      1440      1450      1460      1470      1480
BH 5   TAAGGATGTATAGTCCTACCAGCATTCTGGACATAAGACAAGGACCAAAGGAACCCTTTA
       :::: :::::::: :::::::::::::::::::::::::::::::::::::::::::::
Licuw, TAAGAATGTATAGCCCTACCAGCATTCTGGACATAAGACAAGGACCAAAGGAACCCTTTA
      1620      1630      1640      1650      1660      1670

         1490      1500      1510      1520      1530      1540
BH 5   GAGACTATGTAGACCGGTTCTATAAAACTCTAAGAGCCGAGCAAGCTTCACAGGAAGTAA
       :::: :::::::::::::::::::::::::::::::: ::::::::::::: ::::
Licuw, GAGATTATGTAGACCGGTTCTATAAAACTCTAAGAGCCGAACAAGCTTCACAGGATGTAA
      1680      1690      1700      1710      1720      1730

         1550      1560      1570      1580      1590      1600
BH 5   AAAATTGGATGACAGAAACCTTGTTGGTCCAAAATGCGAACCCAGATTGTAAGACTATTT
       :::::::::::::::::::::::::::::::::::: ::::::::::::::::::::
Licuw, AAAATTGGATGACAGAAACCTTGTTGGTCCAAAATGCAAACCCAGATTGTAAGACTATTT
      1740      1750      1760      1770      1780      1790

         1610      1620      1630      1640      1650      1660
BH 5   TAAAAGCATTGGGACCAGCAGCTACTCTAGAAGAAATGATGACAGCATGTCAGGGAGTGG
       :::::::::::::::::::::::: :::::::::::::::::::::::::::::::::
Licuw, TAAAAGCATTGGGACCAGCAGCTACACTAGAAGAAATGATGACAGCATGTCAGGGAGTGG
      1800      1810      1820      1830      1840      1850

         1670      1680      1690      1700      1710      1720
BH 5   GAGGACCCGGCCATAAAGCAAGAGTTTTGGCTGAAGCAATGAGCCAAGTAACAAATTCAA
       : :::::::::::::::::::::::::::::::: :::::::::::::::::: ::
Licuw, GGGGACCCGGCCATAAAGCAAGAGTTTTGGCTGAAGCCATGAGCCAAGTAACAAATCCAG
      1860      1870      1880      1890      1900      1910

         1730      1740      1750      1760      1770      1780
BH 5   CTACCATAATGATGCAAAGAGGCAATTTTAGGAACCAAAGAAAGATTGTTAAGTGTTTCA
       ::: :::::::::::: :::::::::::::::::::::::::::: ::::::::::::
Licuw, CTAACATAATGATGCAGAGAGGCAATTTTAGGAACCAAAGAAAGACTGTTAAGTGTTTCA
      1920      1930      1940      1950      1960      1970

         1790      1800      1810      1820      1830      1840
BH 5   ATTGTGGCAAAGAAGGGCACATAGCAAGAAATTGCAAGGCCCCTAGAAAAAGAGGCTGTT
       ::::::::::::::::: :::::::: : :::::::: ::::::::: :::: :::  :::
Licuw, ATTGTGGCAAAGAAGG-CACATAGCCAAAAATTGCAGGGCCCCTAGGAAAA-AGG--GTT
      1980      1990       2000      2010      2020       2030

         1850      1860      1870      1880      1890      1900
BH 5   GGAAATGTGGAAAGGAAGGACACCAAATGAAAGATTGTACTGAGAGACAGGCTAATTTTT
       : : :::::::: :::::::::::::::::::::::: :::::::::::::::::::::
Licuw, TGGAGTGTGGAAGGGAAGGACACCAAATGAAAGATTGCACTGAGAGACAGGCTAATTTTT
         2040      2050      2060      2070      2080      2090

         1910      1920      1930      1940      1950      1960
BH 5   TAGGGAAGATCTGGCCTTCCTACAAGGGAAGGCCAGGGAATTTTCTTCAGAGCAGACCAG
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Licuw, TAGGGAAGATCTGGCCTTCCTACAAGGGAAGGCCAGGGAATTTTCTTCAGAGCAGACCAG
         2100      2110      2120      2130      2140      2150

         1970      1980      1990      2000      2010      2020
BH 5   AGCCAACAGCCCCACCATTTCTTCAGAGCAGACCAGAGCCAACAGCCCCACCAGAAGAGA
       ::::::::::::::::                                      :::::::
Licuw, AGCCAACAGCCCCACCA----------------------------------GAAGAGA
         2160      2170

         2030      2040      2050      2060      2070      2080
BH 5   GCTTCAGGTCTGGGGTAGAGACAACAACTCCCTCTCAGAAGCAGGAGCCGATAGACAAGG
       ::::::::: ::::: :::: ::::::::::::::::::::::::::::::::::::::
Licuw, GCTTCAGGTTTGGGGAGGAGAAAACAACTCCCTCTCAGAAGCAGGAGCCGATAGACAAGG
      2180      2190      2200      2210      2220      2230

         2090      2100      2110      2120      2130      2140
BH 5   AACTGTATCCTTTAACTTCCCTCAGATCACTCTTTGGCAACGACCCCTCGTCACAATAAA
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::: ::
Licuw, AACTGTATCCTTTAACTTCCCTCAGATCACTCTTTGGCAACGACCCCTCGTCACAATTAA
      2240      2250      2260      2270      2280      2290
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TABLE II-continued

(BH 5 and 8 v. LUCIW)
89.8% identity

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          2150       2160       2170       2180       2190       2200
BH 5    G-ATAGGGGGGCAACTAAAGGAAGCTCTATTAGATACAGGAGCAGATGATACAGTATTAG
        : ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Licuw, GGATAGGGGGGCAACTAAAGGAAGCTCTATTAGATACAGGAGCAGATGATACAGTATTAG
      2300       2310       2320       2330       2340       2350

          2210       2220       2230       2240       2250       2260
BH 5    AAGAAATGAGTTTGCCAGGAAGATGGAAACCAAAAATGATAGGGGGAATTGGAGGTTTTA
        ::::::::: :::::::::: :::::::::::::::::::::::::::::::::::::::
Licuw, AAGAAATGAATTTGCCAGGAAAATGGAAACCAAAAATGATAGGGGGAATTGGAGGTTTTA
      2360       2370       2380       2390       2400       2410

          2270       2280       2290       2300       2310       2320
BH 5    TCAAAGTAAGACAGTATGATCAGATACTCATAGAAATCTGTGGACATAAAGCTATAGGTA
        :::::::::::::::: ::::::::::   :::::::::::::::::::::::::::::
Licuw, TCAAAGTAAGACAGTACGATCAGATACCTGTAGAAATCTGTGGACATAAAGCTATAGGTA
      2420       2430       2440       2450       2460       2470

          2330       2340       2350       2360       2370       2380
BH 5    CAGTATTAGTAGGACCTACACCTGTCAACATAATTGGAAGAAATCTGTTGACTCAGATTG
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Licuw, CAGTATTAGTAGGACCTACACCTGTCAACATAATTGGAAGAAATCTGTTGACTCAGATTG
      2480       2490       2500       2510       2520       2530

          2390       2400       2410       2420       2430       2440
BH 5    GTTGCACTTTAAATTTTCCCATTAGTCCTATTGAAACTGTACCAGTAAAATTAAAGCCAG
        :::: :::::::::: :::::::::::::::::::::::::::::::::::::::::::
Licuw, GTTGTACTTTAAATTTCCCCATTAGTCCTATTGAAACTGTACCAGTAAAATTAAAGCCAG
      2540       2550       2560       2570       2580       2590

          2450       2460       2470       2480       2490       2500
BH 5    GAATGGATGGCCCAAAAGTTAAACAATGGCCATTGACAGAAGAAAAAATAAAAGCATTAG
        :::::::::::::::::::: ::::::::::::::::::::::::::::::::::::::
Licuw, GAATGGATGGCCCAAAAGTTAAGCAATGGCCATTGACAGAAGAAAAAATAAAAGCATTAG
      2600       2610       2620       2630       2640       2650

          2510       2520       2530       2540       2550       2560
BH 5    TAGAAATTTGTACAGAAATGGAAAAGGAAGGGAAAATTTCAAAAATTGGGCCTGAAAATC
        :::: :: ::::::::::::::::::::::::::::::::::::::::::::::::::::
Licuw, TAGAGATATGTACAGAAATGGAAAAGGAAGGGAAAATTTCAAAAATTGGGCCTGAAAATC
      2660       2670       2680       2690       2700       2710

          2570       2580       2590       2600       2610       2620
BH 5    CATACAATACTCCAGTATTTGCCATAAAGAAAAAAGACAGTACTAAATGGAGAAAATTAG
        :::::::::::::::::::: :::::::::::::::::::::::::::::::: :::
Licuw, CATACAATACTCCAGTATTTGCTATAAAGAAAAAAGACAGTACTAAATGGAGAAAACTAG
      2720       2730       2740       2750       2760       2770

          2630       2640       2650       2660       2670       2680
BH 5    TAGATTTCAGAGAACTTAATAGGAGAACTCAAGACTTCTGGGAAGTTCAATTGGGAATAC
        ::::::::::::::::::::  :::::::::::::::::::::::::: :: :::::::
Licuw, TAGATTTCAGAGAACTTAATAAAAGAACTCAAGACTTCTGGGAAGTTCAGTTAGGAATAC
      2780       2790       2800       2810       2820       2830

          2690       2700       2710       2720       2730       2740
BH 5    CACATCCCGCAGGGTTAAAAAA-GAAAAAATCAGTAACAGTACTGGATGTGGGTGATGCA
        :::: ::::::::::::::::: :::::::::::::::::: ::::::::::::::::
Licuw, CACA-CCCGCAGGGTTAAAAAAAGAAAAAATCAGTAACAGTATTGGATGTGGGTGATGCA
      2840       2850       2860       2870       2880       2890

          2750       2760       2770       2780       2790       2800
BH 5    TATTTTTCAGTTCCCTTAGATGAAGACTTCAGGAAGTATACTGCATTTACCATACCTAGT
        :: :::::::::::::::::: ::::::: :: :::::::::::::::::::::::::::
Licuw, TACTTTTCAGTTCCCTTAGATAAAGACTTTAGAAAGTATACTGCATTTACCATACCTAGT
        2900       2910       2920       2930       2940       2950

          2810       2820       2830       2840       2850       2860
BH 5    ATAAATAATGAGACACCAGGGATTAGATATCAGTACAATGTG-CTTCCACAGGGATGGAA
        ::::: :::::::::::::::::::::::::::::::::: :: ::::::::::::::
Licuw, ATAAACAATGAGACACCAGGGATTAGATATCAGTACAATGTGGCTGCCACAGGGATGGAA
        2960       2970       2980       2990       3000       3010
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TABLE II-continued

(BH 5 and 8 v. LUCIW)
89.8% identity

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            2870       2880       2890       2900       2910       2920
BH 5    AGGATCACCAGCAATATTCCAAAGTAGCATGACAAAAATCTTAGAGCCTTTTAGAAAACA
        :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Licuw,  AGGATCACCAGCAATATTCCAAAGTAGCATGACAAAAATCTTAGAGCCTTTTAGAAAACA
        3020       3030       3040       3050       3060       3070

            2930       2940       2950       2960       2970       2980
BH 5    AAATCCAGACATAGTTATCTATCAATACATGGATGATTTGTATGTAGGATCTGACTTAGA
         :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Licuw,  GAATCCAGACATAGTTATCTATCAATACATGGATGATTTGTATGTAGGATCTGACTTAGA
        3080       3090       3100       3110       3120       3130

            2990       3000       3010       3020       3030       3040
BH 5    AATAGGGCAGCATAGAACAAAAATAGAGGAGCTGAGACAACATCTGTTGAGGTGGGGATT
        ::::::::::::::::::::::::::::: :::::::: ::::::::::::::::::::
Licuw,  AATAGGGCAGCATAGAACAAAAATAGAGGAACTGAGACAGCATCTGTTGAGGTGGGGATT
        3140       3150       3160       3170       3180       3190

            3050       3060       3070       3080       3090       3100
BH 5    TACCACACCAGACAAAAAACATCAGAAAGAACCTCCATTCCTTTGGATGGGTTATGAACT
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Licuw,  TACCACACCAGACAAAAAACATCAGAAAGAACCTCCATTCCTTTGGATGGGTTATGAACT
        3200       3210       3220       3230       3240       3250

            3110       3120       3130       3140       3150       3160
BH 5    CCATCCTGATAAATGGACAGTACAGCCTATAGTGCTGCCAGAAAAAGACAGCTGGACTGT
        :::::::::::::::::::::::::::::: :::::::::::::::::::::::::::::
Licuw,  CCATCCTGATAAATGGACAGTACAGCCTATAATGCTGCCAGAAAAAGACAGCTGGACTGT
        3260       3270       3280       3290       3300       3310

            3170       3180       3190       3200       3210       3220
BH 5    CAATGACATACAGAAGTTAGTGGGAAAATTGAATTGGGCAAGTCAGATTTATCCAGGGAT
        :::::::::::::::::::::::::::::::::::::::::::::::::::: :::::::
Licuw,  CAATGACATACAGAAGTTAGTGGGAAAATTGAATTGGGCAAGTCAGATTTATGCAGGGAT
        3320       3330       3340       3350       3360       3370

            3230       3240       3250       3260       3270       3280
BH 5    TAAAGTAAGGCAATTATGTAAACTCCTTAGAGGAACCAAAGCACTAACAGAAGTAATACC
        :::::::: ::: ::::::::::::::::::::::::::::::::::::::::::::::::
Licuw,  TAAAGTAAAGCAGTTATGTAAACTCCTTAGAGGAACCAAAGCACTAACAGAAGTAATACC
        3380       3390       3400       3410       3420       3430

            3290       3300       3310       3320       3330       3340
BH 5    ACTAACAGAAGAAGCAGAGCTAGAACTGGCAGAAAACAGAGAGATTCTAAAAGAACCAGT
        :::::::::::::::::::::::::::::::::::: :::::::::::::::::::::
Licuw,  ACTAACAGAAGAAGCAGAGCTAGAACTGGCAGAAAACAGGGAGATTCTAAAAGAACCAGT
        3440       3450       3460       3470       3480       3490

            3350       3360       3370       3380       3390       3400
BH 5    ACATGGAGTGTATTATGACCCATCAAAAGACTTAATAGCAGAAATACAGAAGCAGGGGCA
        ::::: ::: :::::::::::::::::::::::: :::::::::::::::::::::::::
Licuw,  ACATGAAGTATATTATGACCCATCAAAAGACTTAGTAGCAGAAATACAGAAGCAGGGGCA
        3500       3510       3520       3530       3540       3550

             3410       3420       3430       3440       3450       3460
BH 5    AGGCCAATGGACATATCAAATTTATCAAGAGCCATTTAAAAATCTGAAAACAGGAAAATA
        :::::::::::::::::::::::::::::::::::::::::::::::::::::::::: ::
Licuw,  AGGCCAATGGACATATCAAATTTATCAAGAGCCATTTAAAAATCTGAAAACAGGAAAGTA
        3560       3570       3580       3590       3600       3610

             3470       3480       3490       3500       3510       3520
BH 5    TGCAAGAATGAGGGGTGCCCACACTAATGATGTAAAACAATTAACAGAGGCAGTGCAAAA
        :::::: ::::::::::::::::::::::::::::::: :::::::::::::::::::
Licuw,  TGCAAGGATGAGGGGTGCCCACACTAATGATGTAAAACAGTTAACAGAGGCAGTGCAAAA
        3620       3630       3640       3650       3660       3670

             3530       3540       3550       3560       3570       3580
BH 5    AATAACCACAGAAAGCATAGTAATATGGGGAAAGACTCCTAAATTTAAACTACCCATACA
        : :: :::::::::::::::::::::::::::::: :::::::::::::::::::::::
Licuw,  AGTATCCACAGAAAGCATAGTAATATGGGGAAAGATTCCTAAATTTAAACTACCCATACA
        3680       3690       3700       3710       3720       3730

             3590       3600       3610       3620       3630       3640
BH 5    AAAAGAAACATGGGAAACATGGTGGACAGAGTATTGGCAAGCCACCTGGATTCCTGAGTG
        ::: :::::::::::: :::::::::  :::::::::::::: ::::::::::::::::
Licuw,  AAAGGAAACATGGGAAGCATGGTGGATGGAGTATTGGCAAGCTACCTGGATTCCTGAGTG
        3740       3750       3760       3770       3780       3790
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TABLE II-continued

(BH 5 and 8 v. LUCIW)
89.8% identity

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           3650       3660       3670       3680       3690       3700
BH 5   GGAGTTTGTTAATACCCCTCCTTTAGTGAAATTATGGTACCAGTTAGAGAAAGAACCCAT
       ::::::::: :::::::::: :::::::::::::::::::::::::::::::::::::
Licuw, GGAGTTTGTCAATACCCCTCCCTTAGTGAAATTATGGTACCAGTTAGAGAAAGAACCCAT
       3800       3810       3820       3830       3840       3850

           3710       3720       3730       3740       3750       3760
BH 5   AGTAGGAGCAGAAACCTTCTATGTAGATGGGGCAGCTAGCAGGGAGACTAAATTAGGAAA
       :::::::::::::: :::::::::::::::::::::  :::::::::::::::::::
Licuw, AGTAGGAGCAGAAACTTTCTATGTAGATGGGGCAGCTAATAGGGAGACTAAATTAGGAAA
       3860       3870       3880       3890       3900       3910

           3770       3780       3790       3800       3810       3820
BH 5   AGCAGGATATGTTACTAATAGAGGAAGACAAAAAGTTGTCACCCTAACTGACACAACAAA
       :::::::::::::::: : :::::::::::::::::::: :: :: ::::::::::::
Licuw, AGCAGGATATGTTACTGACAGAGGAAGACAAAAAGTTGTCTCCATAGCTGACACAACAAA
       3920       3930       3940       3950       3960       3970

           3830       3840       3850       3860       3870       3880
BH 5   TCAGAAGACTGAATTACAAGCAATTCATCTAGCTTTGCAGGATTCGGGATTAGAAGTAAA
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Licuw, TCAGAAGACTGAATTACAAGCAATTCATCTAGCTTTGCAGGATTCGGGATTAGAAGTAAA
       3980       3990       4000       4010       4020       4030

           3890       3900       3910       3920       3930       3940
BH 5   TATAGTAACAGACTCACAATATGCATTAGGAATCATTCAAGCACAACCAGATAAAAGTGA
        :::::::::::::::::::::::::::::::::::::::::::::::::::: :::::
Licuw, CATAGTAACAGACTCACAATATGCATTAGGAATCATTCAAGCACAACCAGATAAGAGTGA
       4040       4050       4060       4070       4080       4090

           3950       3960       3970       3980       3990       4000
BH 5   ATCAGAGTTAGTCAATCAAATAATAGAGCAGTTAATAAAAAAGGAAAAGGTCTATCTGGC
       :::::::::::::: :::::::::::::::::::::::::::::::::: :::::
Licuw, ATCAGAGTTAGTCAGTCAAATAATAGAGCAGTTAATAAAAAAGGAAAAGGTCTACCTGGC
       4100       4110       4120       4130       4140       4150

           4010       4020       4030       4040       4050       4060
BH 5   ATGGGTACCAGCACACAAAGGAATTGGAGGAAATGAACAAGTAGATAAATTAGTCAGTGC
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Licuw, ATGGGTACCAGCACACAAAGGAATTGGAGGAAATGAACAAGTAGATAAATTAGTCAGTGC
       4160       4170       4180       4190       4200       4210

           4070       4080       4090       4100       4110       4120
BH 5   TGGAATCAGGAAAATACTATTTTTAGATGGAATAGATAAGGCCCAAGAAGAACATGAGAA
       :::::::::::::: ::::::::::  ::::::::::::::::::::::::::::::::
Licuw, TGGAATCAGGAAAGTACTATTTTTGAATGGAATAGATAAGGCCCAAGAAGAACATGAGAA
       4220       4230       4240       4250       4260       4270

           4130       4140       4150       4160       4170       4180
BH 5   ATATCACAATAATTGGAGAGCAATGGCTAGTGATTTTAACCTGCCACCTGTAGTAGCAAA
       :::::::: ::::::::::::::::::::::::::::::::::::::::::::::::::
Licuw, ATATCACAGTAATTGGAGAGCAATGGCTAGTGATTTTAACCTGCCACCTGTAGTAGCAAA
       4280       4290       4300       4310       4320       4330

           4190       4200       4210       4220       4230       4240
BH 5   AGAAATAGTAGCCAGCTGTGATAAATGTCAGCTAAAAGGAGAAGCCATGCATGGACAAGT
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Licuw, AGAAATAGTAGCCAGCTGTGATAAATGTCAGCTAAAAGGAGAAGCCATGCATGGACAAGT
       4340       4350       4360       4370       4380       4390

           4250       4260       4270       4280       4290       4300
BH 5/8 AGACTGTAGTCCAGGAATATGGCAACTAGATTGTACACATTTAGAAGGAAAAGTTATCCT
       :::::::::::::::::::::::::::::::::::: :::::::::: :::::::
Licuw, AGACTGTAGTCCAGGAATATGGCAACTAGATTGTACACATCTAGAAGGAAAAATTATCCT
       4400       4410       4420       4430       4440       4450

           4310       4320       4330       4340       4350       4360
BH 5   GGTAGCAGTTCATGTAGCCAGTGGATATATAGAAGCAGAAGTTATTCCAGCAGAAACAGG
       :::::::::::::::::::::::::::::::::::::::::::::::::::: :::::
Licuw, GGTAGCAGTTCATGTAGCCAGTGGATATATAGAAGCAGAAGTTATTCCAGCAGAGACAGG
       4460       4470       4480       4490       4500       4510
```

TABLE II-continued

(BH 5 and 8 v. LUCIW)
89.8% identity

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            4370       4380       4390       4400       4410       4420
BH 5    GCAGGAAACAGCATATTTTCTTTTAAAATTAGCAGGAAGATGGCCAGTAAAAACAATACA
        :::::::::::::::::::: :::::::::::::::::::::::::::::::::::::
Licuw,  GCAGGAAACAGCATATTTTCTCTTAAAATTAGCAGGAAGATGGCCAGTAAAAACAATACA
        4520       4530       4540       4550       4560       4570

            4430       4440       4450       4460       4470       4480
BH 5    TACAGACAATGGCAGCAATTTCACCAGTGCTACGGTTAAGGCCGCCTGTTGGTGGGCGGG
        :::::::::::::::::::::::::: :::::::::::::::::::::::::: ::
Licuw,  TACAGACAATGGCAGCAATTTCACCAGTACTACGGTTAAGGCCGCCTGTTGGTGGGCAGG
        4580       4590       4600       4610       4620       4630

            4490       4500       4510       4520       4530       4540
BH 5    AATCAAGCAGGAATTTGGAATTCCCTACAATCCCCAAAGTCAAGGAGTAGTAGAATCTAT
         ::::::::::::::: :::::::::::::::::::::::::::::::::::::::::
Licuw,  GATCAAGCAGGAATTTGGCATTCCCTACAATCCCCAAAGTCAAGGAGTAGTAGAATCTAT
        4640       4650       4660       4670       4680       4690

            4550       4560       4570       4580       4590       4600
BH 5    GAATAAAGAATTAAAGAAAATTATAGGACAGGTAAGAGATCAGGCTGAACATCTTAAGAC
        :::::: ::::::::::::::::::::::::::::::::::::::::::: ::::::::
Licuw,  GAATAATGAATTAAAGAAAATTATAGGACAGGTAAGAGATCAGGCTGAACACCTTAAGAC
        4700       4710       4720       4730       4740       4750

            4610       4620       4630       4640       4650       4660
BH 5    AGCAGTACAAATGGCAGTATTCATCCACAATTTTAAAAGAAAAGGGGGGATTGGGGGGTA
        :::::::::::::::::::::::::::::::::::::::::::::::::::::::::: ::
Licuw,  AGCAGTACAAATGGCAGTATTCATCCACAATTTTAAAAGAAAAGGGGGGATTGGGGGATA
        4760       4770       4780       4790       4800       4810

            4670       4680       4690       4700       4710       4720
BH 5    CAGTGCAGGGGAAAGAATAGTAGACATAATAGCAACAGACATACAAACTAAAGAATTACA
        :::::::::::::::::::::::::::::::::::::::::::::::::::::::::: ::::
Licuw,  CAGTGCAGGGGAAAGAATAGTAGACATAATAGCAACAGACATACAAACTAAAGAACTACA
        4820       4830       4840       4850       4860       4870

            4730       4740       4750       4760       4770       4780
BH 5    AAAACAAATTACAAAAATTCAAAATTTTCGGGTTTATTACAGGGACAGCAGAAATCCACT
        ::: :::::::::::::::::::::::::::::::::::::::: :: : :::: ::
Licuw,  AAAGCAAATTACAAAAATTCAAAATTTTCGGGTTTATTACAGGGACAACAAAGATCCCCT
        4880       4890       4900       4910       4920       4930

            4790       4800       4810       4820       4830       4840
BH 5    TTGGAAAGGACCAGCAAAGCTCCTCTGGAAAGGTGAAGGGGCAGTAGTAATACAAGATAA
        :::::::::::::::::::: ::::: ::::::::::::::::::::::::::::::::
Licuw,  TTGGAAAGGACCAGCAAAGCTTCTCTGCAAAGGTGAAGGGGCAGTAGTAATACAAGATAA
        4940       4950       4960       4970       4980       4990

            4850       4860       4870       4880       4890       4900
BH 5    TAGTGACATAAAAGTAGTGCCAAGAAGAAAAGCAAAGATCATTAGGGATTATGGAAAACA
        :::::::::::::::::::::::::::::::::::::::::: :::::::::::::::::::::
Licuw,  TAGTGACATAAAAGTAGTGCCAAGAAGAAAAGCAAAAATCATTAGGGATTATGGAAAACA
        5000       5010       5020       5030       5040       5050

             4910       4920       4930       4940       4950       4960
BH 5    GATGGCAGGTGATGATTGTGTGGCAAGTAGACAGGATGAGGATTAGAACATGGAAAAGTT
        ::::::::::::::::::::   ::::::::::::::::::::::::::::::::::::
Licuw,  GATGGCAGGTGATGATTGTGT---AAGTAGACAGGATGAGGATTAGAACATGGAAAAGTT
        5060       5070          5080       5090       5100       5110

             4970       4980       4990       5000       5010       5020
BH 5    TAGTAAAACACCATATGTATGTTTCAGGGAAAGCTAGGGGATGGTTTTATAGACATCACT
        :::::::::::::::::::: :::::  ::::::::  :::::::::: ::: :::::::
Licuw,  TAGTAAAACACCATATGTATATTTCAAAGAAAGCTAAAGGATGGTTTT-TAG-CATCACT
           5120       5130       5140       5150       5160          5170

             5030       5040       5050       5060       5070       5080
BH 5    ATGAAAGCCCTCATCCAAGAATAAGTTCAGAAGTACACATCCCACTAGGGGATGCTAGAT
         ::::::  :::::::::: :::::::::::::::::::: :::::::::::: ::
Licuw,  -TGAAAGTACTCATCCAAGAGTAAGTTCAGAAGTACACATCCCCCTAGGGGATGCTAAAT
              5180       5190       5200       5210       5220       5230

             5090       5100       5110       5120       5130       5140
BH 5    TGGTAATAACAACATATTGGGGTCTGCATACA-GGAGAAAGAGACTGGCATTTGGGTCAG
        :::::::::::::::::::::::::::::: :::::::::: :::::::::: :::
Licuw,  TGGTAATAACAACATATTGGGGTCTGCATACAAGGAGAAAGAGAATGGCATTTGGG-CAG
              5240       5250       5260       5270       5280
```

TABLE II-continued

(BH 5 and 8 v. LUCIW)
89.8% identity

```
            5150       5160       5170       5180       5190       5200
BH 5    GGAGTCTCCATAGAATGGAGGAAAAGGAGATATAGCACACAAGTAGACCCTGAACTAGCA
        :: ::: :::::::::::::: :::     ::  ::::::::::::::::::::  ::::::
Licuw,  GG-GTCGCCATAGAATGGAGAAAA----GAATTAGCACACAAGTAGACCCTGGCCTAGCA
     5290       5300       5310           5320       5330       5340

            5210       5220       5230       5240       5250       5260
BH 5    GACCAACTAATTCATCTGTATTACTTTGATTGTTTTTCAGACTCTGCTATAAGAAAGGCC
        :::::::::::::::::: :::: ::::::::::::::::: :::::::::: ::: :::
Licuw,  GACCAACTAATTCATCTGCATTATTTTGATTGTTTTTCAGAATCTGCTATAAAAAATGCC
          5350       5360       5370       5380       5390       5400

            5270       5280       5290       5300       5310       5320
BH 5    TTATTAGGACACATAGTTAGCCCTAGGTGTGAATATCAAGCAGGACATAACAAGGTAGGA
         :::::::: : : :::::: ::::: ::::::::::::::::::::::::::::::::
Licuw,  ATATTAGGATATAGAGTTAGTCCTAGCTGTGAATATCAAGCAGGACATAACAAGGTAGGA
          5410       5420       5430       5440       5450       5460

              5330       5340       5350       5360       5370       5380
BH 5    TCTCTACAATACTTGGCACTAGCAGCATTAATAACACCAAAAAAGGGAAAGCCACCTTTG
        :::::::::::::::::::::::::::::::::::::::::::  ::::::::::::
Licuw,  TCTCTACAATACTTGGCACTAGCAGCATTAATAACACCAAAAAAGACAAAGCCACCTTTG
          5470       5480       5490       5500       5510       5520

              5390       5400       5410       5420       5430       5440
BH 5    CCTAGTGTTACGAAACTGACAGAGGATAGATGGAACAAGCCCCAGAAGACCAAGGGCCAC
        :::::::::: ::::::::::::::::::::::::::::::::::::::::::::::::
Licuw,  CCTAGTGTTAAGAAACTGACAGAGGATAGATGGAACAAGCCCCAGAAGACCAAGGGCCAC
          5530       5540       5550       5560       5570       5580

              5450       5460       5470       5480       5490       5500
BH 5    AGAGGGAGCCACACAATGAATGGACACTAGAGCTTTTAGAGGAGCTTAAGAATGAAGCTG
        :::::::::: :::::::::::::::::::::::::::::::::::  :::::::
Licuw,  AGAGGGAGCCATACAATGAATGGACACTAGAGCTTTTAGAGGAGCTTAAGAGAGAAGCTG
          5590       5600       5610       5620       5630       5640

              5510       5520       5530       5540       5550       5560
BH 5    TTAGACATTTTCCTAGGATTTGGCTCCATGGCTTAGGGCAACATATCTATGAAACTTATG
        ::::::::::::::::   ::::::::: ::::::: ::: ::::::::::::::::::
Licuw,  TTAGACATTTTCCTAGGCCATGGCTCCATAGCTTAGGACAATATATCTATGAAACTTATG
          5650       5660       5670       5680       5690       5700

              5570       5580       5590       5600       5610       5620
BH 5    GGGATACTTGGGCAGGAGTGGAAGCCATAATAAGAATTCTGCAACAACTGCTGTTTATCC
        :::::::::::::::::::::::::::::::::::::::::::::::::::::::::: :
Licuw,  GGGATACTTGGGCAGGAGTGGAAGCCATAATAAGAATTCTGCAACAACTGCTGTTTATTC
          5710       5720       5730       5740       5750       5760

                5630       5640       5650       5660       5670       5680
BH 5    ATTTTCAGAATTGGGTGTCGACATAGCAGAATAGGCGTTACTCAACAGAGGAGAGCAAGA
        :::: :::::::::::::: ::::::::::::::: ::: ::::::::::::::::::
Licuw,  ATTT-CAGAATTGGGTGTCAACATAGCAGAATAGGCATTATTCAACAGAGGAGAGCAAGA
           5770       5780       5790       5800       5810       5820

                  5690       5700       5710       5720       5730
BH 5    A---ATGGAGCCAGTAGATCCTAGACTAGAGCCCTGGAAGCATCCAGGAAGTCAGCCTAA
        :   ::::::::::::::::::  ::::::::::::::::::::::::::::::::::
Licuw,  AGAAATGGAGCCAGTAGATCCTAATCTAGAGCCCTGGAAGCATCCAGGAAGTCAGCCTAG
           5830       5840       5850       5860       5870       5880

        5740       5750       5760       5770       5780       5790
BH 5    AACTGCTTGTACCACTTGCTATTGTAAAAAGTGTTGCTTTCATTGCCAAGTTTGTTTCAT
         :::::::::: :: :::::::::::::::::::::::::::::: : :  :::::::
Licuw,  GACTGCTTGTAACAATTGCTATTGTAAAAAGTGTTGCTTTCATTGCTACGCGTGTTTCAC
           5890       5900       5910       5920       5930       5940

        5800       5810       5820       5830       5840       5850
BH 5    AACAAAAGCCTTAGGCATCTCCTATGGCAGGAAGAAGCGGAGACAGCGACGAA GAGCTC
        :: ::::: ::::::::::::::::::::::::::::::::::::::::::::::::::
Licuw,  AAGAAAAGGCTTAGGCATCTCCTATGGCAGGAAGAAGCGGAGACAGCGACGAAGAGCTC
           5950       5960       5970       5980       5990       6000
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TABLE II-continued

(BH 5 and 8 v. LUCIW)
89.8% identity

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       5860       5870       5880       5890       5900       5910
BH 8   GAGCTCATCGAAGCAGTCAGACTCATCAAGTTTCTCTATCAAAGCAGTAAGTAGTACATGT
          ::::   ::   :::::::::::::::::: :::::::::::::::::::::::::: ::::
Licuw,---CTCAG-GA--CAGTCAGACTCATCAAGCTTCTCTATCAAAGCAGTAAGTAGTAAATGT
                  6010       6020       6030       6040       6050

      5920       5930          5940       5950       5960       5970
BH 8   AATGCAACCTATACAAATA---GCAATAGTAGCATTAGTAGTAGCAATAATAATAGCAAT
       ::::::: :: ::::::::   ::::::::: :::::::::::: :  ::::::::::::
Licuw, AATGCAATCTTTACAAATATTAGCAATAGTATCATTAGTAGTAGTAGCAATAATAGCAAT
       6060       6070       6080       6090       6100       6110

         5980       5990       6000       6010       6020       6030
BH 8   AGTTGTGTGGTCCATAGTAATCATAGAATATAGGAAAATATTAAGACAAAGAAAAATAGA
       ::::::::::: :::::::: :::::::::::::::::::::::::::::::::: :::::
Licuw, AGTTGTGTGGACCATAGTACTCATAGAATATAGGAAAATATTAAGACAAAGAAAA-TAGA
       6120       6130       6140       6150       6160       6170

         6040       6050       6060       6070       6080       6090
BH 8   CAGGTTAATTGATAGACTAATAGAAAGAGCAGAAGACAGTGGCAATGAGAGTGAAGGAGA
       ::: :::::::::::: ::: ::::: :::::::::::::::::::::: :::::::: ::
Licuw, CAGATTAATTGATAGAATAAGAGAAAAAGCAGAAGACAGTGGCAATGAAAGTGAAGGGGA
       6180       6190       6200       6210       6220       6230

                  6100       6110       6120       6130       6140
BH 8   ---------AATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCACCATGCTCCTTG
                 : ::::::::::::::::::::::            ::::: :::::::::
Licuw, CCAGGAGGAATTATCAGCACTTGTGGAGATGGG------------GCACCTTGCTCCTTG
       6240       6250       6260                    6270       6280

         6150       6160       6170       6180       6190       6200
BH 8   GGATGTTGATGATCTGTAGTGCTACAGAAAAATTGTGGGTCACAGTCTATTTAGGGGTAC
       :::::::::::::::::::::::::::::::::::::::::::: :::: :: ::::
Licuw, GGATGTTGATGATCTGTAGTGCTACAGAAAAATTGTGGGTCACAGTTTATTATGGAGTAC
         6290       6300       6310       6320       6330       6340

         6210       6220       6230       6240       6250       6260
BH 8   CTGTGTGGAAGGAAGCAACCACCACTCTATTTTGTGCATCAGATGCTAAAGCATATGATA
       :::::::::: :::::::: :::::::::::::::::::::::::::: ::::::::::
Licuw, CTGTGTGGAAAGAAGCAACTACCACTCTATTTTGTGCATCAGATGCTAGAGCATATGATA
         6350       6360       6370       6380       6390       6400

         6270       6280       6290       6300       6310       6320
BH 8   CAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCCCAACCCACAAG
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Licuw, CAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCCCAACCCACAAG
         6410       6420       6430       6440       6450       6460

         6330       6340       6350       6360       6370       6380
BH 8   AAGTAGTATTGGTAAATGTGACAGAAAATTTTAACATGTGGAAAAATGACATGGTAGAAC
       :::::::::: :::::::::::::::::::::::::::::::::: ::::::::::::
Licuw, AAGTAGTATTGGGAAATGTGACAGAAAATTTTAACATGTGGAAAAATAACATGGTAGAAC
         6470       6480       6490       6500       6510       6520

         6390       6400       6410       6420       6430       6440
BH 8   AGATGCATGAGGATATAATCAGTTTATGGGATCAAAGCCTAAAGCCATGTGTAAAATTAA
       ::::::: ::::::::::::::::::::::::::::::::::::::::::::::::::::
Licuw, AGATGCAGGAGGATATAATCAGTTTATGGGATCAAAGCCTAAAGCCATGTGTAAAATTAA
         6530       6540       6550       6560       6570       6580

         6450       6460       6470       6480       6490       6500
BH 8   CCCCACTCTGTGTTAGTTTAAAGTGCACTGATTTGAAGAATGATACTAATACCAATAGTA
       :::::::::::::::: :::::: :::::::::::::  ::: : ::::::::::::::::
Licuw, CCCCACTCTGTGTTACTTTAAATTGCACTGATTTGGGGAAGGCTACTAATACCAATAGTA
         6590       6600       6610       6620       6630       6640

         6510       6520       6530       6540       6550       6560
BH 8   GTAGCGGGAGAATGATAATGGAGAAAGGAGAGATAAAAAACTGCTCTTTCAATATCAGCA
       :::   ::: :     :::    :::::::: :::::::::::::::::::::::: ::
Licuw, GTAATTGGAAAGAAGAAATA---AAAGGAGAAATAAAAAACTGCTCTTTCAATATCACCA
         6650       6660          6670       6680       6690       6700

         6570       6580       6590       6600       6610       6620
BH 8   CAAGCAAAAGAGGTAAGGTGCAGAAAGAATATGCATTTTTTTATAAACTTGATATAATAC
       :::::: ::::: :::: : ::::::::: ::::: :::::  ::: :::::: :: :::
Licuw, CAAGCATAAGAGATAAGATTCAGAAAGAAAATGCACTTTTTCGTAACCTTGATGTAGTAC
            6710       6720       6730       6740       6750       6760
```

TABLE II-continued

(BH 5 and 8 v. LUCIW)
89.8% identity

```
        6630      6640            6650              6660      6670
BH 8    CAATAGATAATGATA------CTACCAGCTATAC---------GTTGACAAGTTGTAACA
        :::::::::::: ::      :::::: ::::::         ::::: :  ::::::::
Licuw,  CAATAGATAATGCTAGTACTACTACCAACTATACCAACTATAGGTTGATACATTGTAACA
             6770      6780      6790      6800      6810      6820

             6680      6690      6700      6710      6720      6730
BH 8    CCTCAGTCATTACACAGGCCTGTCCAAAGGTATCCTTTGAGCCAATTCCCATACATTATT
          :::::::::::::::::::::::::::::: :::::::::::::::::::::::::
Licuw,  GATCAGTCATTACACAGGCCTGTCCAAAGGTATCATTTGAGCCAATTCCCATACATTATT
             6830      6840      6850      6860      6870      6880

             6740      6750      6760      6770      6780      6790
BH 8    GTGCCCCGGCTGGTTTTGCGATTCTAAAATGTAATAATAAGACGTTCAATGGAACAGGAC
        :: :::::::::::::::::::::::: :::::::::: :::::::::: ::::::::
Licuw,  GTACCCCGGCTGGTTTTGCGATTCTAAAGTGTAATAATAAAACGTTCAATGGAAAAGGAC
             6890      6900      6910      6920      6930      6940

              6800      6810      6820      6830      6840      6850
BH 8    CATGTACAAATGTCAGCACAGTACAATGTACACATGGAATTAGGCCAGTAGTATCAACTC
        :::::::::::::::::::::::::::::::::::::::::::::::: :::: :::::::
Licuw,  CATGTACAAATGTCAGCACAGTACAATGTACACATGGAATTAGGCCAATAGTGTCAACTC
             6950      6960      6970      6980      6990      7000

               6860      6870      6880      6890      6900
BH 8    AACTG-CTGTTAAATGGCAGTCTAGCAGAAGAAGAGGTAGTAATTAGATCTGTCAATTTC
        ::::: :::::::::::::::::::::::::::::::::::::::::::::: :::::::
Licuw,  AACTGTCTGTTAAATGGCAGTCTAGCAGAAGAAGAGGTAGTAATTAGATCTGACAATTTC
             7010      7020      7030      7040      7050      7060

    6910      6920      6930      6940      6950      6960
BH 8    ACGGACAATGCTAAAACCATAATAGTACAGCTGAACACATCTGTAGAAATTAATTGTACA
        ::: ::::::::::::::::::::::::::::::   :::::::: :::::: ::::::
Licuw,  ACGAACAATGCTAAAACCATAATAGTACAGCTGAATGAATCTGTAGCAATTAACTGTACA
             7070      7080      7090      7100      7110      7120

    6970      6980      6990      7000      7010      7020
BH 8    AGACCCAACAACAATACAAGAAAAAGTATCCAAATCCAGAGGGGACCAGGGAGAGCATTT
        :::::::::::::::::::::::::::::: : ::       ::::::::::::::::::
Licuw,  AGACCCAACAACAATACAAGAAAAAGTATCTATATA------GGACCAGGGAGAGCATTT
             7130      7140      7150            7160      7170

    7030      7040          7050      7060      7070      7080
BH 8    GTTACAATAGGAAAAATA---GGAAATATGAGACAAGCACATTGTAACATTAGTAGAGCA
          ::::: ::::: ::::   ::: :::: ::: :::::::::::::::::::::::::
Licuw,  CATACAACAGGAAGAATAATAGGAGATATAAGAAAAGCACATTGTAACATTAGTAGAGCA
         7180      7190      7200      7210      7220      7230

        7090      7100      7110      7120      7130      7140
BH 8    AAATGGAATGCCACTTTAAAACAGATAGATAGCAAATTAAGAGAACAATTTGGAAATAAT
         ::::::::  ::::::: ::::::::: ::  :::::::::::::: ::::: ::::::
Licuw,  CAATGGAATAACACTTTAGAACAGATAGTTAAAAAATTAAGAGAACAGTTTGGGAATAAT
         7240      7250      7260      7270      7280      7290

        7150      7160      7170      7180      7190      7200
BH 8    AAAACAATAATCTTTAAGCAGTCCTCAGGAGGGGACCCAGAAATTGTAACGCACAGTTTT
        ::::::::: ::::::: :: :::::::::::::::::::::::::::: :::::::::
Licuw,  AAAACAATAGTCTTTAATCAATCCTCAGGAGGGGACCCAGAAATTGTAATGCACAGTTTT
         7300      7310      7320      7330      7340      7350

        7210      7220      7230      7240      7250      7260
BH 8    AATTGTGGAGGGGAATTTTTCTACTGTAATTCAACACAACTGTTTAATAGTACTTGGAGT
        :::::: :::::::::::::::::::::: :::::::::::::::::: ::: :::::
Licuw,  AATTGTAGAGGGGAATTTTTCTACTGTAATACAACACAACTGTTTAATAATACATGGAG-
         7360      7370      7380      7390      7400      7410

        7270      7280      7290                7300      7310
BH 8    ACTAAAGGGTCAAATAACACTGAAGGAAGT---------GACACAATCACCCTCCCATGC
                :: :::: :::::::::::: :          ::::::::::  ::::::::
Licuw,  --------GTTAAATCACACTGAAGGAACTAAAGGAAATGACACAATCATACTCCCATGT
                 7420      7430      7440      7450      7460
```

TABLE II-continued

(BH 5 and 8 v. LUCIW)
89.8% identity

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      7320      7330      7340      7350      7360      7370
BH 8  AGAATAAAACAAATTATAAACATGTGGCAGGAAGTAGGAAAAGCAATGTATGCCCCTCCC
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Licuw, AGAATAAAACAAATTATAAACATGTGGCAGGAAGTAGGAAAAGCAATGTATGCCCCTCCC
      7470      7480      7490      7500      7510      7520

      7380      7390      7400      7410      7420      7430
BH 8  ATCAGTGGACAAATTAGATGTTCATCAAATATTACAGGGCTGCTATTAACAAGAGATGGT
      ::  : :::::::::: ::::::::::::::::::::::::::::::::::::::::::
Licuw, ATTGGAGGACAAATTAGTTGTTCATCAAATATTACAGGGCTGCTATTAACAAGAGATGGT
      7530      7540      7550      7560      7570      7580

      7440         7450      7460      7470      7480      7490
BH 8  GGTAATA--GCAAC-AATGAGTCCGAGATCTTCAGACCTGGAGGAGGAGATATGAGGGAC
      ::::  :  : ::: ::::: ::::: ::::::::::::::::::::::::::::::::
Licuw, GGTACAAATGTAACTAATGACACCGAGGTCTTCAGACCTGGAGGAGGAGATATGAGGGAC
      7590      7600      7610      7620      7630      7640

        7500      7510      7520      7530      7540      7550
BH 8  AATTGGAGAAGTGAATTATATAAATATAAAGTAGTAAAAATTGAACCATTAGGAGTAGCA
      :::::::::::::::::::::::::::::::: :::::::::::::::::: :::::
Licuw, AATTGGAGAAGTGAATTATATAAATATAAAGTAATAAAAATTGAACCATTAGGAATAGCA
      7650      7660      7670      7680      7690      7700

        7560      7570      7580      7590      7600         7610
BH 8   CCCACCAAGGCAAAGAGAAGAGTGGTGCAGAGAGAAAAAAGAGCAGTGGGAATAG---GA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::   ::
Licuw, CCCACCAAGGCAAAGAGAAGAGTGGTGCAGAGAGAAAAAAGAGCAGTGGGAATAGTAGGA
      7710      7720      7730      7740      7750      7760

           7620      7630      7640      7650      7660      7670
BH 8  GCTTTGTTCCTTGGGTTCTTGGGAGCAGCAGGAAGCACTATGGGCGCAGCGTCAATGACG
      ::: ::::::::::::::::::::::::::::::::::::: :::: :::: :::::
Licuw, GCTATGTTCCTTGGGTTCTTGGGAGCAGCAGGAAGCACTATGGGGGCAGTGTCATTGACG
      7770      7780      7790      7800      7810      7820

           7680      7690      7700      7710      7720      7730
BH 8  CTGACGGTACAGGCCAGACAATTATTGTCTGGTATAGTGCAGCAGCAGAACAATTTGCTG
      ::::::::::::::::::::::::::::::::::::: ::::::::::::::::::
Licuw, CTGACGGTACAGGCCAGACAATTATTGTCTGGTATAGTGCAACAGCAGAACAATTTGCTG
      7830      7840      7850      7860      7870      7880

           7740      7750      7760      7770      7780       7790
BH 8  AGGGCTATTGAGGGCCAACAGCATCTGTTGCAACTCACAGTCTGGGGCATCA-GCAGCTC
      ::::::::::::  ::::: :::::::::::::::::::::::::::::: :::::::
Licuw, AGGGCTATTGAGGCGCAACAACATCTGTTGCAACTCACAGTCTGGGGCATCAAGCAGCTC
      7890      7900      7910      7920      7930      7940

            7800      7810      7820      7830      7840      7850
BH 8  CAGGCAAGAATCCTGGCTGTGGAAAGATACCTAAAGGATCAACAGCTCCTGGGGATTTGG
      ::::::::: ::::::::::::::::::::::::: ::::::::::::::   :::::::
Licuw, CAGGCAAGAGTCCTGGCTGTGGAAAGATACCTAAGGGATCAACAGCTCCTA--GATTTGG
      7950      7960      7970      7980      7990         8000

           7860      7870      7880      7890      7900      7910
BH 8  GGTTGCTCTGGAAAACTCATTTGCACCACTGCTGTGCCTTGGAATGCTAGTTGGAGTAAT
      ::: :::::::::: ::::::::::::::::::::::::::::::::::::::::::::
Licuw, GGT-GCTCTGGAAA-CTCATTTGCACCACTGCTGTGCCTTGGAATGCTAGTTGGAGTAAT
         8010      8020      8030      8040      8050      8060

           7920      7930      7940      7950      7960      7970
BH 8  AAATCTCTGGAACAGATTTGGAATAACATGACCTGGATGGAGTGGGACAGAGAAATTAAC
      :::::::::::: : :::::: :::::::::::::: ::: ::::::: ::::::::: ::
Licuw, AAATCTCTGGAAGACATTTGGGATAACATGACCTG-ATGCAGTGGGAAAGAGAAATTGAC
          8070      8080      8090       8100      8110      8120

           7980      7990      8000      8010      8020      8030
BH 8  AATTACACAAGCTTAATACACTCCTTAATTGAAGAATCGCAAAACCAGCAAGAAAAGAAT
      :::::::::: :  :::: :: ::::: :::::::::::: ::::: ::::::::::::
Licuw, AATTACACAAACACAATATACACCTTACTTGAAGAATCGCAGAACCAACAAGAAAAGAAT
           8130      8140      8150      8160      8170      8180

           8040      8050      8060      8070      8080      8090
BH 8  GAACAAGAATTATTGGAATTAGATAAATGGGCAAGTTTGTGGAATTGGTTTAACATAACA
      :::::::::::::: ::::: ::::: :::::::::::::::::::::::::: :::::::
Licuw, GAACAAGAATTATTAGAATTGGATAAGTGGGCAAGTTTGTGGAATTGGTTTAGCATAACA
           8190      8200      8210      8220      8230      8240
```

TABLE II-continued

(BH 5 and 8 v. LUCIW)
89.8% identity

```
            8100      8110      8120      8130      8140      8150
BH 8    AATTGGCTGTGGTATATAAAATTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAGA
        :: ::::::::::::::::  :::::::::::::::::::::::::::::::::::::
Licuw,  AACTGGCTGTGGTATATAAAGATATTCATAATGATAGTAGGAGGCTTGGTAGGTTTAAGA
             8250      8260      8270      8280      8290      8300

            8160      8170      8180      8190      8200      8210
BH 8    ATAGTTTTTGCTGTACTTTCTATAGTGAATAGAGTTAGGCAGGGATATTCACCATTATCG
        :::::::::::::: :::::::::::::::::::::::::::::::: :::::::: ::
Licuw,  ATAGTTTTTGCTGTGCTTTCTATAGTGAATAGAGTTAGGCAGGGATACTCACCATTGTCA
             8310      8320      8330      8340      8350      8360

            8220      8230      8240      8250      8260      8270
BH 8    TTTCAGACCCACCTCCCAAACCCGAGGGGACCCGACAGGCCCGAAGGAATAGAAGAAGAA
        ::::::::::  ::::::   :::::   ::::::::: ::::: ::::: :::::::::
Licuw,  TTTCAGACCCGGCTCCCAGTGCCGAG---ACCCGACAG-CCCGACGGAATCGAAGAAGAA
            8370      8380        8390      8400      8410

            8280      8290      8300      8310      8320      8330
BH 8    GGTGGAGAGAGAGACAGAGACAGATCCATTCGATTAGTGAACGGATCCTTAGCACTTATC
        :: ::::::::::::::::::::::: :::::::::: : :::: ::::::::::::
Licuw,  GG-GGAGAGAGAGACAGAGACAGATCCGTTCGATTAGTGGATGGATTCTTAGCACTTATC
        8420      8430      8440      8450      8460      8470

            8340      8350      8360      8370      8380      8390
BH 8    TGGGACGATCTGCGGAGCCTGTGCCTCTTCAGCTACCACCGCTTGAGAGACTTACTCTTG
        ::::: ::::::::::::::::::::::::::::::  :: ::::::::::::::::::
Licuw,  TGGGAAGATCTGCGGAGCCTGTGCCTCTTCAGCTACCGGCGGTTGAGAGACTTACTCTTG
        8480      8490      8500      8510      8520      8530

            8400      8410      8420      8430      8440      8450
BH 8    ATTGTAACGAGGATTGTGGAACTTCTGGGACGCAGGGGGTGGGAAGCCCTCAAATATTGG
        :::: : :::::: ::::::: ::::::: : :::::::::::   ::::::::::::
Licuw,  ATTGCAGCGAGGACTGTGGAAATTCTGGGGCACAGGGGGTGGGAA---CTCAAATATTGG
        8540      8550      8560      8570      8580          8590

            8460      8470      8480      8490      8500      8510
BH 8    TGGAATCTCCTACAGTATTGGAGTCAGGAACTAAAGAATAGTGCTGTTAACTTGCTCAAT
        :::: :::::: :::::::::: :::::::::::::::::::::::::: :: ::::::
Licuw,  TGGAGTCTCCTGCAGTATTGGATTCAGGAACTAAAGAATAGTGCTGTTAGCTGGCTCAAC
           8600      8610      8620      8630      8640      8650

            8520      8530      8540      8550      8560      8570
BH 8    GCCACAGCCATAGCAGTAGCTGAGGGGACAGATAGGGTTATAGAAGTATTACAAGCAGCT
        :::::::: ::::::::: :::::::::::::::::::::::::::::  ::::  ::::
Licuw,  GCCACAGCTATAGCAGTAACTGAGGGGACAGATAGGGTTATAGAAGTAGCACAAAGAGCT
           8660      8670      8680      8690      8700      8710

              8580      8590      8600      8610      8620      8630
BH 8    TATAGAGCCATTCGCCACATACCTAGAAGAATAAGACAGGGCTTGGAAAGGATTTTGCTA
        :::::::: :::: :::::::: ::::::::: :::::   :::::::::: ::::::::
Licuw,  TATAGAGCTATTCTCCACATACATAGAAGAATTAGACA---CTTGGAAAGGCTTTTGCTA
           8720      8730      8740      8750          8760      8770

              8640      8650      8660      8670      8680      8690
BH 8    TAAGATGGGTGGCAAGTGGTCAAAAAGTAGTGTGGTTGGATGGCCTGCTGTAAGGGAAAG
        ::::::::: :   :::::::::: : ::: :::  :::::: ::::: ::::::::::
Licuw,  TAAGATGGGGG---AGTGGTCAAAACG-AGTATGGG-GGATGGTCTGCTATAAGGGAAAG
              8780          8790        8800        8810      8820

              8700                    8710      8720      8730
BH 8    AATGAGACGAGCTGAGCCA-----------GCAGCAGATGGGGTGGGAGCAGTATCTCG
        ::::::::::::::::::             :::::::::::::::::: ::::::::::
Licuw,  AATGAGACGAGCTGAGCCACGAGCTGAGCCAGCAGCAGATGGG-TGGGA-CAGTATCTCG
         8830      8840      8850      8860        8870        8880

      8740      8750      8760      8770      8780      8790
BH 8    AGACCTAGAAAAACATGGAGCAATCACAAGTAGCAATACAGCAGCTACCAATGCTGATTG
        :::::: ::::::::::::  :::::::::::::::::::::::::::: ::::::::::
Licuw,  AGACCTGGAAAAACATGGA--AATCACAAGTAGCAATACAGCAGCTACTAATGCTGATTG
           8890      8900        8910      8920      8930      8940
```

TABLE II-continued

(BH 5 and 8 v. LUCIW)
89.8% identity

```
     8800      8810      8820      8830      8840      8850
BH 8   TGCTTGGCTAGAAGCACAAGAGGAGGAGGAGGTGGGTTTTCCAGTCACACCTCAGGTACC
       ::: :::::::::::::::::::::: :::::::::::::::::: ::::::::::::
Licuw, TGCCTGGCTAGAAGCACAAGAGGAGGAAGAGGTGGGTTTTCCAGTCAGACCTCAGGTACC
            8950      8960      8970      8980      8990      9000

     8860      8870      8880      8890      8900      8910
BH 8   TTTAAGACCAATGACTTACAAGGCAGCTGTAGATCTTAGCCACTTTTTAAAAGAAAAGGG
       :::::::::::::::::::::::::::: ::::: ::::::::::::::::::::::::
Licuw, TTTAAGACCAATGACTTACAAGGCAGCTTTAGATATTAGCCACTTTTTAAAAGAAAAGGG
            9010      9020      9030      9040      9050      9060

     8920      8930      8940      8950      8960      8970
BH 8   GGGACTGGAAGGGCTAATTCACTCCCAACGAAGACAAGATATCCTTGATCTGTGGATCCA
       ::::::::::::::::::   :::::: :::::::::: ::::::::::::::::: :
Licuw, GGGACTGGAAGGGCTAATTTGGTCCCAAAGAAGACAAGAGATCCTTGATCTGTGGATCTA
            9070      9080      9090      9100      9110      9120

     8980      8990      9000      9010      9020      9030
BH 8   CCACACACAAGGCTACTTCCCTGATTGGCAGAACTACACACCAGGGCCAGGGATCAGATA
       :::::::::::::::::::::::::::::::: ::::::::::::::::::::::::
Licuw, CCACACACAAGGCTACTTCCCTGATTGGCAGAATTACACACCAGGGCCAGGGATCAGATA
            9130      9140      9150      9160      9170      9180

     9040      9050      9060      9070      9080      9090
BH 8   TCCACTGACCTTTGGATGGTGCTACAAGCTAGTACCAGTTGAGCCAGAGAAGATAGAAGA
       :::::::::::::::::::::: :::::::::::::::::::::::::::: :::::::
Licuw, TCCACTGACCTTTGGATGGTGCTTCAAGCTAGTACCAGTTGAGCCAGAGAAGGTAGAAGA
            9190      9200      9210      9220      9230      9240

     9100      9110      9120      9130      9140      9150
BH 8   AGCCAATAAAGGAGAGAACACCAGCTTGTTACACCCTGTGAGCCTGCATGGGATGGATGA
        :::::: ::::::::::::  :::::::::::::: :::::::::::::::::: ::
Licuw, GGCCAATGAAGGAGAGAACAA-AGCTTGTTACACCCTATGAGCCTGCATGGGATGGAGGA
            9250      9260       9270      9280      9290      9300

     9160      9170      9180      9190      9200      9210
BH 8   CCCTGAGAGAGAAGTGTTAGAGTGGAGGTTTGACAGCCGCCTAGCATTTCATCACATGGC
       : : :::: :::::::::: ::::::::::::::   ::::::::::::::::::::
Licuw, CGCGGAGAAAGAAGTGTTAGTGTGGAGGTTTGACAGCAAACTAGCATTTCATCACATGGC
             9310      9320      9330      9340      9350      9360

     9220      9230      9240      9250      9260      9270
BH 8   CCGAGAGCTGCATCCGGAGTACTTCAAGAACTGCTGACATCGAGCTTGCTACAAGGGACT
       ::::::::::::::::::::::: :::  :::::::::::::::::: ::::::::::::
Licuw, CCGAGAGCTGCATCCGGAGTACTACAAAGACTGCTGACATCGAGCTTTCTACAAGGGACT
             9370      9380      9390      9400      9410      9420

     9280      9290              9300      9310      9320      9330
BH 8   TTCCGCTGGGGACTTT--------GCGTGGCCTGGGCGGGACTGGGGAGTGGCGAGCCCT
       ::::::::::::::::        :::::::::::::::::::::::::::::::  ::::
Licuw, TTCCGCTGGGGACTTTCCAGGGAGGCGTGGCCTGGGCGGGACTGGGGAGTGGCGT-CCCT
             9430      9440      9450      9460      9470

             9340              9350      9360      9370      9380
BH 8   CAGATCCTGCATATAA--------TTTTTGCCTGTACTGGGTCTCTCTGGTTAGACCAGA
       ::::::::::::::::        :::::::::::::::::::::::::::::::::::
Licuw, CAGATGCTGCATATAAGCAGCTGCTTTTTGCCTGTACTGGGTCTCTCTGGTTAGACCAGA
    9480      9490      9500      9510      9520      9530

           9390
BH 8   TCTGAGCCTGGGAGCTC----------------------------------------------
       :::::::::::::::::
Licuw, TCTGAGCCTGGGAGCTCTCTGGCTAACTAGGGAACCCACTGCTTAAGCCTCAATAAAGCT
    9540      9550      9560      9570      9580      9590

       ------------------------------------------------------------

Licuw, TGCCTTGAGTGCTTCAAGTAGTGTGTGCCCGTCTGTTGTGTGACTCTGGTAACTAGAGAT
    9600      9610      9620      9630      9640      9650

       ----------------------------------------

Licuw, CCCTCAGACCCTTTTAGTCAGTGTGGAAAAATCTCTAGCAG
    9660      9670      9680      9690      9700
```

TABLE III

(BH 10 v. LUCIW)
90.0% identity

```
                10        20        30        40        50
BH 10  -TGGAAGGGCTAATTCACTCCCAACGAAGACAAGATATCCTTGATCTGTGGATCTACCAC
        :::::::::::::    :::::: :::::::::: ::::::::::::::::::::::::
Licuw, CTGGAAGGGCTAATTTGGTCCCAAAGAAGACAAGAGATCCTTGATCTGTGGATCTACCAC
               10        20        30        40        50        60

      60        70        80        90       100       110
BH 10  ACACAAGGCTACTTCCCTGATTAGCAGAACTACACACCAGGGCCAGGGATCAGATATCCA
       :::::::::::::::::::::: :::::: ::::::::::::::::::::::::::::::
Licuw, ACACAAGGCTACTTCCCTGATTGGCAGAATTACACACCAGGGCCAGGGATCAGATATCCA
               70        80        90       100       110       120

     120       130       140       150       160       170
BH 10  CTGACCTTTGGATGGTGCTACAAGCTAGTACCAGTTGAGCCAGAGAAGTTAGAAGAAGCC
       :::::::::::::::::: :::::::::::::::::::::::::::: ::::::: :::
Licuw, CTGACCTTTGGATGGTGCTTCAAGCTAGTACCAGTTGAGCCAGAGAAGGTAGAAGAGGCC
              130       140       150       160       170       180

     180       190       200       210       220       230
BH 10  AACAAAGGAGAGAACACCAGCTTGTTACACCCTGTGAGCCTGCATGGAATGGATGACCCG
       ::  :::::::::::: ::::::::::::::: :::::::::::: ::::: ::: ::
Licuw, AATGAAGGAGAGAACAACAGCTTGTTACACCCTATGAGCCTGCATGGGATGGAGGACGCG
              190       200       210       220       230       240

     240       250       260       270       280       290
BH 10  GAGAGAGAAGTGTTAGAGTGGAGGTTTGACAGCCGCCTAGCATTTCATCACATGGCCCGA
       :::: :::::::::: ::::::::::::::   ::::::::::::::::::::::::
Licuw, GAGAAAGAAGTGTTAGTGTGGAGGTTTGACAGCAAACTAGCATTTCATCACATGGCCCGA
              250       260       270       280       290       300

     300       310       320       330       340       350
BH 10  GAGCTGCATCCGGAGTACTTCAAGAACTGCTGACATCGAGCTTGCTACAAGGGACTTTCC
       :::::::::::::::::: :::  ::::::::::::::::: ::::::::::::::::
Licuw, GAGCTGCATCCGGAGTACTACAAAGACTGCTGACATCGAGCTTTCTACAAGGGACTTTCC
              310       320       330       340       350       360

     360       370       380       390       400       410
BH 10  GCTGGGGACTTTCCAGGGAGGCGTGGCCTGGGCGGGACTGGGGAGTGGCGAGCCCTCAGA
       :::::::::::::::::::::::::::::::::::::::::::::::::  ::::::::
Licuw, GCTGGGGACTTTCCAGGGAGGCGTGGCCTGGGCGGGACTGGGGAGTGGCGT-CCCTCAGA
              370       380       390       400       410

     420       430        440       450       460       470
BH 10  TCCTGCATATAAGCAG-CTGCTTTTTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATCT
       : ::::::::::::: :::::::::::::::::::::::::::::::::::::::::::
Licuw, TGCTGCATATAAGCAGACTGCTTTTTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATCT
     420       430       440       450       460       470

      480       490
BH 10  GAGCCTGGGAGCTC----------------------------------------------
       :::::::::::::
Licuw, GAGCCTGGGAGCTCTCTGGCTAACTAGGGAACCCACTGCTTAAGCCTCAATAAAGCTTGC
     480       490       500       510       520       530

       ------------------------------------------------------------

Licuw, CTTGAGTGCTTCAAGTAGTGTGTGCCCGTCTGTTGTGTGACTCTGGTAACTAGAGATCCC
     540       550       560       570       580       590

       ------------------------------------------------------------

Licuw, TCAGACCCTTTTAGTCAGTGTGGAAAAATCTCTAGCAGTGGCGCCCGAACAGGGACGCGA
     600       610       620       630       640       650

                                500       510       520       530
BH 10  --------------------GAGCTCTCTCGACGCAGGACTCGGCTTGCTGAAGCGCGCA
                            :::::::::::::::::::::::::::::::::::::
Licuw, AAGCGAAAGTAGAACCAGAGGAGCTCTCTCGACGCAGGACTCGGCTTGCTGAAGCGCGCA
     660       670       680       690       700       710

            540       550       560       570       580       590
BH 10  CGGCAAGAGGCGAGGGGCGGCGACTGGTGAGTACGCCAAAAATTTTGACTAGCGGAGGCT
       : ::::::::::::::::::::::::::::::::::   :::::::::::::::::
Licuw, CAGCAAGAGGCGAGGGGCGGCGACTGGTGAGTACGCCAA--TTTTTGACTAGCGGAGGCT
     720       730       740       750         760       770
```

TABLE III-continued

(BH 10 v. LUCIW)
90.0% identity

```
            600         610         620         630         640         650
BH 10   AGAAGGAGAGAGA--TGGGTGCGAGAGCGTCAGTATTAAGCGGGGGAGAATTAGATCGAT
        ::::::::::::  ::::::::::::::::: ::::::::::::::::::::::::  ::
Licuw,  AGAAGGAGAGAGAGATGGGTGCGAGAGCGTCGGTATTAAGCGGGGGAGAATTAGATAAAT
        780         790         800         810         820         830

              660         670         680         690         700         710
BH 10   GGGAAAAAATTCGGTTAAGGCCAGGGGGAAAGAAAAAATATAAATTAAAACATATAGTAT
        :::::::::::::::::::::::::::::::::::::::::: ::::::::::::::::
Licuw,  GGGAAAAAATTCGGTTAAGGCCAGGGGGAAAGAAAAAATATAAGTTAAAACATATAGTAT
        840         850         860         870         880         890

              720         730         740         750         760         770
BH 10   GGGCAAGCAGGGAGCTAGAACGATTCGCAGTTAATCCTGGCCTGTTAGAAACATCAGAAG
        :::::::::::::::::::::::::::::: :::::::::::::::::::::::::::
Licuw,  GGGCAAGCAGGGAGCTAGAACGATTCGCAGTCAATCCTGGCCTGTTAGAAACATCAGAAG
        900         910         920         930         940         950

              780         790         800         810         820         830
BH 10   GCTGTAGACAAATACTGGGACAGCTACAACCATCCCTTCAGACAGGATCAGAAGAACTTA
        :::: ::::::::: :::::::::::: ::::::::::::::::::::::::::::::
Licuw,  GCTGCAGACAAATATTGGGACAGCTACAGCCATCCCTTCAGACAGGATCAGAAGAACTTA
        960         970         980         990        1000        1010

              840         850         860         870         880         890
BH 10   GATCATTATATAATACAGTAGCAACCCTCTATTGTGTGCATCAAAGGATAGAGATAAAAG
        ::::::::::::::::::::::::::::::::::::::::: :::::::::::::  ::::::
Licuw,  GATCATTATATAATACAGTAGCAACCCTCTATTGTGTACATCAAAGGATAGATGTAAAAG
       1020        1030        1040        1050        1060        1070

              900         910         920         930         940         950
BH 10   ACACCAAGGAAGCTTTAGACAAGATAGAGGAAGAGCAAAACAAAAGTAAGAAAAAAGCAC
        :::::::::::::::::: :::::::::::::::::::::::::::::::::: ::::
Licuw,  ACACCAAGGAAGCTTTAGAGAAGATAGAGGAAGAGCAAAACAAAAGTAAGAAAAAGGCAC
       1080        1090        1100        1110        1120        1130

            960                 970         980         990        1000
BH 10   AGCAAGCAGCAGCTGA------CACAGGACACAGCAGTCAGGTCAGCCAAAATTACCCTA
        ::::::::::::::       ::::::: ::::::: ::::::::::::::::::::::
Licuw,  AGCAAGCAGCAGCTGCAGCTGGCACAGGAAACAGCAGCCAGGTCAGCCAAAATTACCCTA
       1140        1150        1160        1170        1180        1190

          1010        1020        1030        1040        1050        1060
BH 10   TAGTGCAGAACATCCAGGGGCAAATGGTACATCAGGCCATATCACCTAGAACTTTAAATG
        :::::::::: : ::::::::::::::::::::::::::::::::::::::::::::::
Licuw,  TAGTGCAGAACCTACAGGGGCAAATGGTACATCAGGCCATATCACCTAGAACTTTAAATG
       1200        1210        1220        1230        1240        1250

          1070        1080        1090        1100        1110        1120
BH 10   CATGGGTAAAAGTAGTAGAAGAGAAGGCTTTCAGCCCAGAAGTAATACCCATGTTTTCAG
        :::::::::::::::::::: :::::::::::::::::::::::::::::::::::::::
Licuw,  CATGGGTAAAAGTAGTAGAAGAAAAGGCTTTCAGCCCAGAAGTAATACCCATGTTTTCAG
       1260        1270        1280        1290        1300        1310

          1130        1140        1150        1160        1170        1180
BH 10   CATTATCAGAAGGAGCCACCCCACAAGATTTAAACACCATGCTAAACACAGTGGGGGGAC
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Licuw,  CATTATCAGAAGGAGCCACCCCACAAGATTTAAACACCATGCTAAACACAGTGGGGGGAC
       1320        1330        1340        1350        1360        1370

          1190        1200        1210        1220        1230        1240
BH 10   ATCAAGCAGCCATGCAAATGTTAAAAGAGACCATCAATGAGGAAGCTGCAGAATGGGATA
        :::::::::::::::::::::::::::::: :::::::::::::::::::::::::::
Licuw,  ATCAAGCAGCCATGCAAATGTTAAAAGAGACTATCAATGAGGAAGCTGCAGAATGGGATA
       1380        1390        1400        1410        1420        1430

          1250        1260        1270        1280        1290        1300
BH 10   GAGTACATCCAGTGCATGCAGGGCCTATTGCACCAGGCCAGATGAGAGAACCAAGGGGAA
        :::: ::::::::::::::::::::::::::::::::: ::::::::::::::::::
Licuw,  GAGTGCATCCAGTGCATGCAGGGCCTATTGCACCAGGCCAAATGAGAGAACCAAGGGGAA
       1440        1450        1460        1470        1480        1490

          1310        1320        1330        1340        1350        1360
BH 10   GTGACATAGCAGGAACTACTAGTACCCTTCAGGAACAAATAGGATGGATGACAAATAATC
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Licuw,  GTGACATAGCAGGAACTACTAGTACCCTTCAGGAACAAATAGGATGGATGACAAATAATC
       1500        1510        1520        1530        1540        1550
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TABLE III-continued

(BH 10 v. LUCIW)
90.0% identity

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         1370      1380      1390      1400      1410      1420
BH 10  CACCTATCCCAGTAGGAGAAATTTATAAAAGATGGATAATCCTGGGATTAAATAAAATAG
       :::::::::::::::::::: :::::::::::::::::::::::::::::::::::::
Licuw, CACCTATCCCAGTAGGAGAAATCTATAAAAGATGGATAATCCTGGGATTAAATAAAATAG
      1560      1570      1580      1590      1600      1610

         1430      1440      1450      1460      1470      1480
BH 10  TAAGAATGTATAGCCCTACCAGCATTCTGGACATAAGACAAGGACCAAAAGAACCTTTTA
       :::::::::::::::::::::::::::::::::::::::::::::::::: ::::: ::::
Licuw, TAAGAATGTATAGCCCTACCAGCATTCTGGACATAAGACAAGGACCAAAGGAACCCTTTA
      1620      1630      1640      1650      1660      1670

         1490      1500      1510      1520      1530      1540
BH 10  GAGACTATGTAGACCGGTTCTATAAAACTCTAAGAGCCGAGCAAGCTTCACAGGAGGTAA
       :::: ::::::::::::::::::::::::::::::::: ::::::::::::: ::::
Licuw, GAGATTATGTAGACCGGTTCTATAAAACTCTAAGAGCCGAACAAGCTTCACAGGATGTAA
      1680      1690      1700      1710      1720      1730

         1550      1560      1570      1580      1590      1600
BH 10  AAAATTGGATGACAGAAACCTTGTTGGTCCAAAATGCGAACCCAGATTGTAAGACTATTT
       :::::::::::::::::::::::::::::::::: ::::::::::::::::::::
Licuw, AAAATTGGATGACAGAAACCTTGTTGGTCCAAAATGCAAACCCAGATTGTAAGACTATTT
      1740      1750      1760      1770      1780      1790

         1610      1620      1630      1640      1650      1660
BH 10  TAAAAGCATTGGGACCAGCGGCTACACTAGAAGAAATGATGACAGCATGTCAGGGAGTAG
       :::::::::::::::::: :::::::::::::::::::::::::::::::::::::: :
Licuw, TAAAAGCATTGGGACCAGCAGCTACACTAGAAGAAATGATGACAGCATGTCAGGGAGTGG
      1800      1810      1820      1830      1840      1850

         1670      1680      1690      1700      1710      1720
BH 10  GAGGACCCGGCCATAAGGCAAGAGTTTTGGCTGAAGCAATGAGCCAAGTAACAAATACAG
       : :::::::::::::: :::::::::::::::::: :::::::::::::::::: :::
Licuw, GGGGACCCGGCCATAAAGCAAGAGTTTTGGCTGAAGCCATGAGCCAAGTAACAAATCCAG
      1860      1870      1880      1890      1900      1910

         1730      1740      1750      1760      1770      1780
BH 10  CTACCATAATGATGCAGAGAGGCAATTTTAGGAACCAAAGAAAGATGGTTAAGTGTTTCA
       ::: ::::::::::::::::::::::::::::::::::::::  ::::::::::::
Licuw, CTAACATAATGATGCAGAGAGGCAATTTTAGGAACCAAAGAAAGACTGTTAAGTGTTTCA
      1920      1930      1940      1950      1960      1970

         1790      1800      1810      1820      1830      1840
BH 10  ATTGTGGCAAAGAAGGGCACACAGCCAGAAATTGCAGGGCCCCTAGGAAAAAGGGCTGTT
       ::::::::::::::: :::: ::::: :::::::::::::::::::::::::::   ::
Licuw, ATTGTGGCAAAGAAGG-CACATAGCCAAAAATTGCAGGGCCCCTAGGAAAAAGGG---TT
      1980      1990       2000      2010      2020      2030

         1850      1860      1870      1880      1890      1900
BH 10  GGAAATGTGGAAAGGAAGGACACCAAATGAAAGATTGTACTGAGAGACAGGCTAATTTTT
        : : ::::::: ::::::::::::::::::::::: :::::::::::::::::::::
Licuw, TGGAGTGTGGAAGGGAAGGACACCAAATGAAAGATTGCACTGAGAGACAGGCTAATTTTT
         2040      2050      2060      2070      2080      2090

         1910      1920      1930      1940      1950      1960
BH 10  TAGGGAAGATCTGGCCTTCCTACAAGGGAAGGCCAGGGAATTTTCTTCAGAGCAGACCAG
       ::::::::::::::::::::::::::::::::::::::::::::::
Licuw, TAGGGAAGATCTGGCCTTCCTACAAGGGAAGGCCAGGGAATTTTCT--------------
         2100      2110      2120      2130

         1970      1980      1990      2000      2010      2020
BH 10  AGCCAACAGCCCCACCATTTCTTCAGAGCAGACCAGAGCCAACAGCCCCACCAGAAGAGA
                           ::::::::::::::::::::::::::::::::::::
Licuw, ----------------------TCAGAGCAGACCAGAGCCAACAGCCCCACCAGAAGAGA
                        2140      2150      2160      2170

         2030      2040      2050      2060      2070      2080
BH 10  GCTTCAGGTCTGGGGTAGAGACAACAACTCCCCCTCAGAAGCAGGAGCCGATAGACAAGG
       ::::::::: :::::  :::: :::::::::: :::::::::::::::::::::::::::
Licuw, GCTTCAGGTTTGGGGAGGAGAAAACAACTCCCTCTCAGAAGCAGGAGCCGATAGACAAGG
      2180      2190      2200      2210      2220      2230
```

TABLE III-continued

(BH 10 v. LUCIW)
90.0% identity

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         2090      2100      2110      2120      2130      2140
BH 10  AACTGTATCCTTTAACTTCCCTCAGATCACTCTTTGGCAACGACCCCTCGTCACAATAAA
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::: ::
Licuw, AACTGTATCCTTTAACTTCCCTCAGATCACTCTTTGGCAACGACCCCTCGTCACAATTAA
      2240      2250      2260      2270      2280      2290

          2150      2160      2170      2180      2190      2200
BH 10  G-ATAGGGGGGCAACTAAAGGAAGCTCTATTAGATACAGGAGCAGATGATACAGTATTAG
       : ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Licuw, GGATAGGGGGGCAACTAAAGGAAGCTCTATTAGATACAGGAGCAGATGATACAGTATTAG
      2300      2310      2320      2330      2340      2350

          2210      2220      2230      2240      2250      2260
BH 10  AAGAAATGAGTTTGCCAGGAAGATGGAAACCAAAAATGATAGGGGGAATTGGAGGTTTTA
       ::::::::: :::::::::: :::::::::::::::::::::::::::::::::::::
Licuw, AAGAAATGAATTTGCCAGGAAAATGGAAACCAAAAATGATAGGGGGAATTGGAGGTTTTA
      2360      2370      2380      2390      2400      2410

          2270      2280      2290      2300      2310      2320
BH 10  TCAAAGTAAGACAGTATGATCAGATACTCATAGAAATCTGTGGACATAAAGCTATAGGTA
       ::::::::::::::: :::::::::   ::::::::::::::::::::::::::::::
Licuw, TCAAAGTAAGACAGTACGATCAGATACCTGTAGAAATCTGTGGACATAAAGCTATAGGTA
      2420      2430      2440      2450      2460      2470

          2330      2340      2350      2360      2370      2380
BH 10  CAGTATTAGTAGGACCTACACCTGTCAACATAATTGGAAGAAATCTGTTGACTCAGATTG
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Licuw, CAGTATTAGTAGGACCTACACCTGTCAACATAATTGGAAGAAATCTGTTGACTCAGATTG
      2480      2490      2500      2510      2520      2530

          2390      2400      2410      2420      2430      2440
BH 10  GTTGCACTTTAAATTTTCCCATTAGCCCTATTGAGACTGTACCAGTAAAATTAAAGCCAG
       :::: :::::::::: :::::::: :::::::: ::::::::::::::::::::::::
Licuw, GTTGTACTTTAAATTTCCCCATTAGTCCTATTGAAACTGTACCAGTAAAATTAAAGCCAG
      2540      2550      2560      2570      2580      2590

          2450      2460      2470      2480      2490      2500
BH 10  GAATGGATGGCCCAAAAGTTAAACAATGGCCATTGACAGAAGAAAAAATAAAAGCATTAG
       :::::::::::::::::::: ::::::::::::::::::::::::::::::::::::::
Licuw, GAATGGATGGCCCAAAAGTTAAGCAATGGCCATTGACAGAAGAAAAAATAAAAGCATTAG
      2600      2610      2620      2630      2640      2650

          2510      2520      2530      2540      2550      2560
BH 10  TAGAAATTTGTACAGAAATGGAAAAGGAAGGGAAAATTTCAAAAATTGGGCCTGAGAATC
       :::: :: ::::::::::::::::::::::::::::::::::::::::::::: ::::
Licuw, TAGAGATATGTACAGAAATGGAAAAGGAAGGGAAAATTTCAAAAATTGGGCCTGAAAATC
      2660      2670      2680      2690      2700      2710

          2570      2580      2590      2600      2610      2620
BH 10  CATACAATACTCCAGTATTTGCCATAAAGAAAAAAGACAGTACTAAATGGAGAAAATTAG
       ::::::::::::::::::::: :::::::::::::::::::::::::::::::::: :::
Licuw, CATACAATACTCCAGTATTTGCTATAAAGAAAAAAGACAGTACTAAATGGAGAAAACTAG
      2720      2730      2740      2750      2760      2770

          2630      2640      2650      2660      2670      2680
BH 10  TAGATTTCAGAGAACTTAATAAGAGAACTCAAGACTTCTGGGAAGTTCAATTAGGAATAC
       :::::::::::::::::::::: :::::::::::::::::::::::::: ::::::::::
Licuw, TAGATTTCAGAGAACTTAATAAAAGAACTCAAGACTTCTGGGAAGTTCAGTTAGGAATAC
      2780      2790      2800      2810      2820      2830

          2690      2700       2710      2720      2730      2740
BH 10  CACATCCCGCAGGGTTAAAAAA-GAAAAAATCAGTAACAGTACTGGATGTGGGTGATGCA
       :::: ::::::::::::::::: :::::::::::::::::: ::::::::::::::::::
Licuw, CACA-CCCGCAGGGTTAAAAAAAGAAAAAATCAGTAACAGTATTGGATGTGGGTGATGCA
      2840       2850      2860      2870      2880      2890

           2750      2760      2770      2780      2790      2800
BH 10  TATTTTTCAGTTCCCTTAGATGAAGACTTCAGGAAGTATACTGCATTTACCATACCTAGT
       :: ::::::::::::::::: ::::::: :: :::::::::::::::::::::::::::
Licuw, TACTTTTCAGTTCCCTTAGATAAAGACTTTAGAAAGTATACTGCATTTACCATACCTAGT
       2900      2910      2920      2930      2940      2950

           2810      2820      2830      2840       2850      2860
BH 10  ATAAACAATGAGACACCAGGGATTAGATATCAGTACAATGTG-CTTCCACAGGGATGGAA
       :::::::::::::::::::::::::::::::::::::::: :: ::::::::::::::
Licuw, ATAAACAATGAGACACCAGGGATTAGATATCAGTACAATGTGGCTGCCACAGGGATGGAA
       2960      2970      2980      2990      3000      3010
```

TABLE III-continued

(BH 10 v. LUCIW)
90.0% identity

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           2870       2880       2890       2900       2910       2920
BH 10  AGGATCACCAGCAATATTCCAAAGTAGCATGACAAAAATCTTAGAGCCTTTTAAAAAACA
       :::::::::::::::::::::::::::::::::::::::::::::::::::: ::::::
Licuw, AGGATCACCAGCAATATTCCAAAGTAGCATGACAAAAATCTTAGAGCCTTTTAGAAAACA
       3020       3030       3040       3050       3060       3070

           2930       2940       2950       2960       2970       2980
BH 10  AAATCCAGACATAGTTATCTATCAATACATGGATGATTTGTATGTAGGATCTGACTTAGA
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Licuw, GAATCCAGACATAGTTATCTATCAATACATGGATGATTTGTATGTAGGATCTGACTTAGA
       3080       3090       3100       3110       3120       3130

           2990       3000       3010       3020       3030       3040
BH 10  AATAGGGCAGCATAGAACAAAAATAGAGGAGCTGAGACAACATCTGTTGAGGTGGGGACT
       :::::::::::::::::::::::::::: :::::::: ::::::::::::::::: :
Licuw, AATAGGGCAGCATAGAACAAAAATAGAGGAACTGAGACAGCATCTGTTGAGGTGGGGATT
       3140       3150       3160       3170       3180       3190

           3050       3060       3070       3080       3090       3100
BH 10  TACCACACCAGACAAAAAACATCAGAAAGAACCTCCATTCCTTTGGATGGGTTATGAACT
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Licuw, TACCACACCAGACAAAAAACATCAGAAAGAACCTCCATTCCTTTGGATGGGTTATGAACT
       3200       3210       3220       3230       3240       3250

           3110       3120       3130       3140       3150       3160
BH 10  CCATCCTGATAAATGGACAGTACAGCCTATAGTGCTGCCAGAAAAAGACAGCTGGACTGT
       :::::::::::::::::::::::::::: :::::::::::::::::::::::::::::
Licuw, CCATCCTGATAAATGGACAGTACAGCCTATAATGCTGCCAGAAAAAGACAGCTGGACTGT
       3260       3270       3280       3290       3300       3310

           3170       3180       3190       3200       3210       3220
BH 10  CAATGACATACAGAAGTTAGTGGGGAAATTGAATTGGGCAAGTCAGATTTACCCAGGGAT
       ::::::::::::::::::::::: :::::::::::::::::::::::  :::::::
Licuw, CAATGACATACAGAAGTTAGTGGGAAAATTGAATTGGGCAAGTCAGATTTATGCAGGGAT
       3320       3330       3340       3350       3360       3370

           3230       3240       3250       3260       3270       3280
BH 10  TAAAGTAAGGCAATTATGTAAACTCCTTAGAGGAACCAAAGCACTAACAGAAGTAATACC
       :::::::: ::: ::::::::::::::::::::::::::::::::::::::::::::::
Licuw, TAAAGTAAAGCAGTTATGTAAACTCCTTAGAGGAACCAAAGCACTAACAGAAGTAATACC
       3380       3390       3400       3410       3420       3430

           3290       3300       3310       3320       3330       3340
BH 10  ACTAACAGAAGAAGCAGAGCTAGAACTGGCAGAAAACAGAGAGATTCTAAAAGAACCAGT
       :::::::::::::::::::::::::::::::::::: ::::::::::::::::::::
Licuw, ACTAACAGAAGAAGCAGAGCTAGAACTGGCAGAAAACAGGGAGATTCTAAAAGAACCAGT
       3440       3450       3460       3470       3480       3490

           3350       3360       3370       3380       3390       3400
BH 10  ACATGGAGTGTATTATGACCCATCAAAAGACTTAATAGCAGAAATACAGAAGCAGGGGCA
       ::::: ::: :::::::::::::::::::::::: :::::::::::::::::::::::::
Licuw, ACATGAAGTATATTATGACCCATCAAAAGACTTAGTAGCAGAAATACAGAAGCAGGGGCA
       3500       3510       3520       3530       3540       3550

           3410       3420       3430       3440       3450       3460
BH 10  AGGCCAATGGACATATCAAATTTATCAAGAGCCATTTAAAAATCTGAAAACAGGAAAATA
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::: ::
Licuw, AGGCCAATGGACATATCAAATTTATCAAGAGCCATTTAAAAATCTGAAAACAGGAAAGTA
       3560       3570       3580       3590       3600       3610

           3470       3480       3490       3500       3510       3520
BH 10  TGCAAGAATGAGGGGTGCCCACACTAATGATGTAAAACAATTAACAGAGGCAGTGCAAAA
       :::::: :::::::::::::::::::::::::::::: ::::::::::::::::::::
Licuw, TGCAAGGATGAGGGGTGCCCACACTAATGATGTAAAACAGTTAACAGAGGCAGTGCAAAA
       3620       3630       3640       3650       3660       3670

           3530       3540       3550       3560       3570       3580
BH 10  AATAACCACAGAAAGCATAGTAATATGGGGAAAGACTCCTAAATTTAAACTACCCATACA
       : :: ::::::::::::::::::::::::::::: :::::::::::::::::::::::::
Licuw, AGTATCCACAGAAAGCATAGTAATATGGGGAAAGATTCCTAAATTTAAACTACCCATACA
       3680       3690       3700       3710       3720       3730
```

TABLE III-continued

(BH 10 v. LUCIW)
90.0% identity

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            3590       3600       3610       3620       3630       3640
BH 10   AAAGGAAACATGGGAAACATGGTGGACAGAGTATTGGCAAGCCACCTGGATTCCTGAGTG
        ::::::::::::::::: :::::::::  :::::::::::::: ::::::::::::::::
Licuw,  AAAGGAAACATGGGAAGCATGGTGGATGGAGTATTGGCAAGCTACCTGGATTCCTGAGTG
        3740       3750       3760       3770       3780       3790

            3650       3660       3670       3680       3690       3700
BH 10   GGAGTTTGTTAATACCCCTCCTTTAGTGAAATTATGGTACCAGTTAGAGAAAGAACCCAT
        ::::::::: :::::::::: :::::::::::::::::::::::::::::::::::::
Licuw,  GGAGTTTGTCAATACCCCTCCCTTAGTGAAATTATGGTACCAGTTAGAGAAAGAACCCAT
        3800       3810       3820       3830       3840       3850

            3710       3720       3730       3740       3750       3760
BH 10   AGTAGGAGCAGAAACCTTCTATGTAGATGGGGCAGCTAACAGGGAGACTAAATTAGGAAA
        :::::::::::::::: ::::::::::::::::::::::: :::::::::::::::::::
Licuw,  AGTAGGAGCAGAAACTTTCTATGTAGATGGGGCAGCTAATAGGGAGACTAAATTAGGAAA
        3860       3870       3880       3890       3900       3910

            3770       3780       3790       3800       3810       3820
BH 10   AGCAGGATATGTTACTAACAAAGGAAGACAAAAGGTTGTCCCCCTAACTAACACAACAAA
        :::::::::::::::: ::: :::::::::::: :::::: :: :: :: ::::::::::
Licuw,  AGCAGGATATGTTACTGACAGAGGAAGACAAAAAGTTGTCTCCATAGCTGACACAACAAA
        3920       3930       3940       3950       3960       3970

            3830       3840       3850       3860       3870       3880
BH 10   TCAGAAAACTGAGTTACAAGCAATTTATCTAGCTTTGCAGGATTCAGGATTAGAAGTAAA
        :::::: ::::: :::::::::::: :::::::::::::::::: ::::::::::::::
Licuw,  TCAGAAGACTGAATTACAAGCAATTCATCTAGCTTTGCAGGATTCGGGATTAGAAGTAAA
        3980       3990       4000       4010       4020       4030

            3890       3900       3910       3920       3930       3940
BH 10   CATAGTAACAGACTCACAATATGCATTAGGAATCATTCAAGCACAACCAGATAAAAGTGA
        :::::::::::::::::::::::::::::::::::::::::::::::::::::: :::::
Licuw,  CATAGTAACAGACTCACAATATGCATTAGGAATCATTCAAGCACAACCAGATAAGAGTGA
        4040       4050       4060       4070       4080       4090

            3950       3960       3970       3980       3990       4000
BH 10   ATCAGAGTTAGTCAATCAAATAATAGAGCAGTTAATAAAAAAGGAAAAGGTCTATCTGGC
        :::::::::::::: :::::::::::::::::::::::::::::::::::: :::::
Licuw,  ATCAGAGTTAGTCAGTCAAATAATAGAGCAGTTAATAAAAAAGGAAAAGGTCTACCTGGC
        4100       4110       4120       4130       4140       4150

            4010       4020       4030       4040       4050       4060
BH 10   ATGGGTACCAGCACACAAAGGAATTGGAGGAAATGAACAAGTAGATAAATTAGTCAGTGC
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Licuw,  ATGGGTACCAGCACACAAAGGAATTGGAGGAAATGAACAAGTAGATAAATTAGTCAGTGC
        4160       4170       4180       4190       4200       4210

            4070       4080       4090       4100       4110       4120
BH 10   TGGAATCAGGAAAATACTATTTTTAGATGGAATAGATAAGGCCCAAGATGAACATGAGAA
        :::::::::::: ::::::::::  :::::::::::::::::::: ::::::::::::
Licuw,  TGGAATCAGGAAAGTACTATTTTTGAATGGAATAGATAAGGCCCAAGAAGAACATGAGAA
        4220       4230       4240       4250       4260       4270

            4130       4140       4150       4160       4170       4180
BH 10   ATATCACAGTAATTGGAGAGCAATGGCTAGTGATTTTAACCTGCCACCTGTAGTAGCAAA
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Licuw,  ATATCACAGTAATTGGAGAGCAATGGCTAGTGATTTTAACCTGCCACCTGTAGTAGCAAA
        4280       4290       4300       4310       4320       4330

            4190       4200       4210       4220       4230       4240
BH 10   AGAAATAGTAGCCAGCTGTGATAAATGTCAGCTAAAAGGAGAAGCCATGCATGGACAAGT
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Licuw,  AGAAATAGTAGCCAGCTGTGATAAATGTCAGCTAAAAGGAGAAGCCATGCATGGACAAGT
        4340       4350       4360       4370       4380       4390

            4250       4260       4270       4280       4290       4300
BH 10   AGACTGTAGTCCAGGAATATGGCAACTAGATTGTACACATTTAGAAGGAAAAGTTATCCT
        :::::::::::::::::::::::::::::::::::: :::::::::: ::::::: :::
Licuw,  AGACTGTAGTCCAGGAATATGGCAACTAGATTGTACACATCTAGAAGGAAAAATTATCCT
        4400       4410       4420       4430       4440       4450

            4310       4320       4330       4340       4350       4360
BH 10   GGTAGCAGTTCATGTAGCCAGTGGATATATAGAAGCAGAAGTTATTCCAGCAGAAACAGG
        :::::::::::::::::::::::::::::::::::::::::::::::::::::: :::::
Licuw,  GGTAGCAGTTCATGTAGCCAGTGGATATATAGAAGCAGAAGTTATTCCAGCAGAGACAGG
        4460       4470       4480       4490       4500       4510
```

TABLE III-continued

(BH 10 v. LUCIW)
90.0% identity

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           4370       4380       4390       4400       4410       4420
BH 10  GCAGGAAACAGCATATTTTCTTTTAAAATTAGCAGGAAGATGGCCAGTAAAAACAATACA
       :::::::::::::::::::: :::::::::::::::::::::::::::::::::::::::
Licuw, GCAGGAAACAGCATATTTTCTCTTAAAATTAGCAGGAAGATGGCCAGTAAAAACAATACA
       4520       4530       4540       4550       4560       4570

           4430       4440       4450       4460       4470       4480
BH 10  TACAGACAATGGCAGCAATTTCACCAGTGCTACGGTTAAGGCCGCCTGTTGGTGGGCGGG
       :::::::::::::::::::::::::: :::::::::::::::::::::::::::: ::
Licuw, TACAGACAATGGCAGCAATTTCACCAGTACTACGGTTAAGGCCGCCTGTTGGTGGGCAGG
       4580       4590       4600       4610       4620       4630

           4490       4500       4510       4520       4530       4540
BH 10  AATCAAGCAGGAATTTGGAATTCCCTACAATCCCCAAAGTCAAGGAGTAGTAGAATCTAT
        ::::::::::::::: :::::::::::::::::::::::::::::::::::::::::::
Licuw, GATCAAGCAGGAATTTGGCATTCCCTACAATCCCCAAAGTCAAGGAGTAGTAGAATCTAT
       4640       4650       4660       4670       4680       4690

           4550       4560       4570       4580       4590       4600
BH 10  GAATAAAGAATTAAAGAAAATTATAGGACAGGTAAGAGATCAGGCTGAACATCTTAAGAC
       :::::: ::::::::::::::::::::::::::::::::::::::::::: ::::::::
Licuw, GAATAATGAATTAAAGAAAATTATAGGACAGGTAAGAGATCAGGCTGAACACCTTAAGAC
       4700       4710       4720       4730       4740       4750

           4610       4620       4630       4640       4650       4660
BH 10  AGCAGTACAAATGGCAGTATTCATCCACAATTTTAAAAGAAAAGGGGGGATTGGGGGGTA
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::: ::
Licuw, AGCAGTACAAATGGCAGTATTCATCCACAATTTTAAAAGAAAAGGGGGGATTGGGGGATA
       4760       4770       4780       4790       4800       4810

           4670       4680       4690       4700       4710       4720
BH 10  CAGTGCAGGGGAAAGAATAGTAGACATAATAGCAACAGACATACAAACTAAAGAATTACA
       :::::::::::::::::::::::::::::::::::::::::::::::::::: ::::
Licuw, CAGTGCAGGGGAAAGAATAGTAGACATAATAGCAACAGACATACAAACTAAAGAACTACA
       4820       4830       4840       4850       4860       4870

           4730       4740       4750       4760       4770       4780
BH 10  AAAACAAATTACAAAAATTCAAAATTTTCGGGTTTATTACAGGGACAGCAGAAATCCACT
       ::: :::::::::::::::::::::::::::::::::::::::: :: : :::: ::
Licuw, AAAGCAAATTACAAAAATTCAAAATTTTCGGGTTTATTACAGGGACAACAAAGATCCCCT
       4880       4890       4900       4910       4920       4930

           4790       4800       4810       4820       4830       4840
BH 10  TTGGAAAGGACCAGCAAAGCTCCTCTGGAAAGGTGAAGGGGCAGTAGTAATACAAGATAA
       :::::::::::::::::::: ::::: ::::::::::::::::::::::::::::::::
Licuw, TTGGAAAGGACCAGCAAAGCTTCTCTGCAAAGGTGAAGGGGCAGTAGTAATACAAGATAA
       4940       4950       4960       4970       4980       4990

           4850       4860       4870       4880       4890       4900
BH 10  TAGTGACATAAAAGTAGTGCCAAGAAGAAAAGCAAAGATCATTAGGGATTATGGAAAACA
       :::::::::::::::::::::::::::::::::: ::::::::::::::::::::::::
Licuw, TAGTGACATAAAAGTAGTGCCAAGAAGAAAAGCAAAAATCATTAGGGATTATGGAAAACA
       5000       5010       5020       5030       5040       5050

           4910       4920       4930       4940       4950       4960
BH 10  GATGGCAGGTGATGATTGTGTGGCAAGTAGACAGGATGAGGATTAGAACATGGAAAAGTT
       ::::::::::::::::::::   ::::::::::::::::::::::::::::::::::::
Licuw, GATGGCAGGTGATGATTGTGT---AAGTAGACAGGATGAGGATTAGAACATGGAAAAGTT
       5060       5070          5080       5090       5100       5110

           4970       4980       4990       5000       5010       5020
BH 10  TAGTAAAACACCATATGTATGTTTCAGGGAAAGCTAGGGGATGGTTTTATAGACATCACT
       :::::::::::::::::::: :::::  ::::::::  ::::::::::  ::: :::::::
Licuw, TAGTAAAACACCATATGTATATTTCAAAGAAAGCTAAAGGATGGTTTT-TAG-CATCACT
          5120       5130       5140       5150       5160          5170

           5030       5040       5050       5060       5070       5080
BH 10  ATGAAAGCCCTCATCCAAGAATAAGTTCAGAAGTACACATCCCACTAGGGGATGCTAGAT
        ::::::  :::::::::::: ::::::::::::::::::::::: :::::::::::: ::
Licuw, -TGAAAGTACTCATCCAAGAGTAAGTTCAGAAGTACACATCCCCCTAGGGGATGCTAAAT
             5180       5190       5200       5210       5220       5230
```

TABLE III-continued

(BH 10 v. LUCIW)
90.0% identity

```
            5090       5100       5110       5120       5130       5140
BH 10   TGGTAATAACAACATATTGGGGTCTGCATACA-GGAGAAAGAGACTGGCATTTGGGTCAG
        :::::::::::::::::::::::::::::::: :::::::::: :::::::::: :::
Licuw,  TGGTAATAACAACATATTGGGGTCTGCATACAAGGAGAAAGAGAATGGCATTTGGG-CAG
              5240       5250       5260       5270       5280

              5150       5160       5170       5180       5190       5200
BH 10   GGAGTCTCCATAGAATGGAGGAAAAAGAGATATAGCACACAAGTAGACCCTGAACTAGCA
        :: ::: ::::::::::::  :::::: :: ::::::::::::::::::::  ::::::
Licuw,  GG-GTCGCCATAGAATGGAG--AAAAGA-AT-TAGCACACAAGTAGACCCTGGCCTAGCA
     5290       5300       5310       5320       5330       5340

              5210       5220       5230       5240       5250       5260
BH 10   GACCAACTAATTCATCTGTATTACTTTGACTGTTTTTCAGACTCTGCTATAAGAAAGGCC
        :::::::::::::::::: :::: ::::: :::::::::: :::::::::: ::: :::
Licuw,  GACCAACTAATTCATCTGCATTATTTTGATTGTTTTTCAGAATCTGCTATAAAAAATGCC
          5350       5360       5370       5380       5390       5400

              5270       5280       5290       5300       5310       5320
BH 10   TTATTAGGACACATAGTTAGCCCTAGGTGTGAATATCAAGCAGGACATAACAAGGTAGGA
         :::::::: : :::::: ::::: ::::::::::::::::::::::::::::::::::
Licuw,  ATATTAGGATATAGAGTTAGTCCTAGCTGTGAATATCAAGCAGGACATAACAAGGTAGGA
          5410       5420       5430       5440       5450       5460

              5330       5340       5350       5360       5370       5380
BH 10   TCTCTACAATACTTGGCACTAGCAGCATTAATAACACCAAAAAAGATAAAGCCACCTTTG
        :::::::::::::::::::::::::::::::::::::::::::: ::::::::::::
Licuw,  TCTCTACAATACTTGGCACTAGCAGCATTAATAACACCAAAAAAGACAAAGCCACCTTTG
          5470       5480       5490       5500       5510       5520

              5390       5400       5410       5420       5430       5440
BH 10   CCTAGTGTTACGAAACTGACAGAGGATAGATGGAACAAGCCCCAGAAGACCAAGGGCCAC
        :::::::::: ::::::::::::::::::::::::::::::::::::::::::::::::
Licuw,  CCTAGTGTTAAGAAACTGACAGAGGATAGATGGAACAAGCCCCAGAAGACCAAGGGCCAC
          5530       5540       5550       5560       5570       5580

              5450       5460       5470       5480       5490       5500
BH 10   AGAGGGAGCCACACAATGAATGGACACTAGAGCTTTTAGAGGAGCTTAAGAATGAAGCTG
        :::::::::: :::::::::::::::::::::::::::::::::::::  :::::::
Licuw,  AGAGGGAGCCATACAATGAATGGACACTAGAGCTTTTAGAGGAGCTTAAGAGAGAAGCTG
          5590       5600       5610       5620       5630       5640

              5510       5520       5530       5540       5550       5560
BH 10   TTAGACATTTTCCTAGGATTTGGCTCCATGGCTTAGGGCAACATATCTATGAAACTTATG
        :::::::::::::::::   ::::::::: ::::::: ::: ::::::::::::::::::
Licuw,  TTAGACATTTTCCTAGGCCATGGCTCCATAGCTTAGGACAATATATCTATGAAACTTATG
          5650       5660       5670       5680       5690       5700

              5570       5580       5590       5600       5610       5620
BH 10   GGGATACTTGGGCAGGAGTGGAAGCCATAATAAGAATTCTGCAACAACTGCTGTTTATCC
        :::::::::::::::::::::::::::::::::::::::::::::::::::::::::: :
Licuw,  GGGATACTTGGGCAGGAGTGGAAGCCATAATAAGAATTCTGCAACAACTGCTGTTTATTC
          5710       5720       5730       5740       5750       5760

                 5630       5640       5650       5660       5670       5680
BH 10   ATTTTCAGAATTGGGTGTCGACATAGCAGAATAGGCGTTACTCGACAGAGGAGAGCAAGA
        :::: :::::::::::::: ::::::::::::::::: ::: :: ::::::::::::::::
Licuw,  ATTT-CAGAATTGGGTGTCAACATAGCAGAATAGGCATTATTCAACAGAGGAGAGCAAGA
           5770       5780       5790       5800       5810       5820

                    5690       5700       5710       5720       5730
BH 10   A---ATGGAGCCAGTAGATCCTAGACTAGAGCCCTGGAAGCATCCAGGAAGTCAGCCTAA
        :   ::::::::::::::::::  ::::::::::::::::::::::::::::::::::
Licuw,  AGAAATGGAGCCAGTAGATCCTAATCTAGAGCCCTGGAAGCATCCAGGAAGTCAGCCTAG
           5830       5840       5850       5860       5870       5880

         5740       5750       5760       5770       5780       5790
BH 10   AACTGCTTGTACCAATTGCTATTGTAAAAAGTGTTGCTTTCATTGCCAAGTTTGTTTCAT
         :::::::::: :::::::::::::::::::::::::::::::::: : :  :::::::
Licuw,  GACTGCTTGTAACAATTGCTATTGTAAAAAGTGTTGCTTTCATTGCTACGCGTGTTTCAC
           5890       5900       5910       5920       5930       5940

         5800       5810       5820       5830       5840       5850
BH 10   AACAAAAGCCTTAGGCATCTCCTATGGCAGGAAGAAGCGGAGACAGCGACGAAGACCTCC
        :: ::::: :::::::::::::::::::::::::::::::::::::::::::::: ::::
Licuw,  AAGAAAAGGCTTAGGCATCTCCTATGGCAGGAAGAAGCGGAGACAGCGACGAAGAGCTCC
           5950       5960       5970       5980       5990       6000
```

TABLE III-continued

(BH 10 v. LUCIW)
90.0% identity

```
      5860       5870       5880       5890       5900       5910
BH 10  TCAAGGCAGTCAGACTCATCAAGTTTCTCTATCAAAGCAGTAAGTAGTACATGTAATGCA
       ::: : ::::::::::::::::: :::::::::::::::::::::::::: ::::::::::
Licuw, TCAGGACAGTCAGACTCATCAAGCTTCTCTATCAAAGCAGTAAGTAGTAAATGTAATGCA
          6010       6020       6030       6040       6050       6060

      5920       5930          5940       5950       5960       5970
BH 10  ACCTATACAAATA---GCAATAGTAGCATTAGTAGTAGCAATAATAATAGCAATAGTTGT
       : :: ::::::::   ::::::::: :::::::::::: :  ::::::::::::::::::
Licuw, ATCTTTACAAATATTAGCAATAGTATCATTAGTAGTAGTAGCAATAATAGCAATAGTTGT
          6070       6080       6090       6100       6110       6120

        5980       5990       6000       6010       6020       6030
BH 10  GTGGTCCATAGTAATCATAGAATATAGGAAAATATTAAGACAAAGAAAAATAGACAGGTT
       :::: :::::::: :::::::::::::::::::::::::::::::::: ::::::: ::
Licuw, GTGGACCATAGTACTCATAGAATATAGGAAAATATTAAGACAAAGAAAA-TAGACAGATT
          6130       6140       6150       6160       6170       6180

        6040       6050       6060       6070       6080
BH 10  AATTGATAGACTAATAGAAAGAGCAGAAGACAGTGGCAATGAGAGTGAAGGAGA------
       :::::::::: ::: ::::: :::::::::::::::::::: :::::::: ::
Licuw, AATTGATAGAATAAGAGAAAAAGCAGAAGACAGTGGCAATGAAAGTGAAGGGGACCAGGA
          6190       6200       6210       6220       6230       6240

        6090       6100       6110       6120       6130       6140
BH 10  ---AATATCAGCACTTGTGGAGATGGGGGTGGAGATGGGGCACCATGCTCCTTGGGATGT
         : ::::::::::::::::::::::            :::: ::::::::::::::
Licuw, GGAATTATCAGCACTTGTGGAGATGGGG------------CACCTTGCTCCTTGGGATGT
          6250       6260       6270                  6280       6290

        6150       6160       6170       6180       6190       6200
BH 10  TGATGATCTGTAGTGCTACAGAAAAATTGTGGGTCACAGTCTATTATGGGGTACCTGTGT
       :::::::::::::::::::::::::::::::::::: :::::::: ::::::::::
Licuw, TGATGATCTGTAGTGCTACAGAAAAATTGTGGGTCACAGTTTATTATGGAGTACCTGTGT
             6300       6310       6320       6330       6340       6350

        6210       6220       6230       6240       6250       6260
BH 10  GGAAGGAAGCAACCACCACTCTATTTTGTGCATCAGATGCTAAAGCATATGATACAGAGG
       :::: :::::::: :::::::::::::::::::::::::::: ::::::::::::::::
Licuw, GGAAAGAAGCAACTACCACTCTATTTTGTGCATCAGATGCTAGAGCATATGATACAGAGG
             6360       6370       6380       6390       6400       6410

        6270       6280       6290       6300       6310       6320
BH 10  TACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCCCAACCCACAAGAAGTAG
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Licuw, TACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCCCAACCCACAAGAAGTAG
             6420       6430       6440       6450       6460       6470

        6330       6340       6350       6360       6370       6380
BH 10  TATTGGTAAATGTGACAGAAAATTTTAACATGTGGAAAAATGACATGGTAGAACAGATGC
       :::::: :::::::::::::::::::::::::::::::: ::::::::::::::::::
Licuw, TATTGGGAAATGTGACAGAAAATTTTAACATGTGGAAAAATAACATGGTAGAACAGATGC
             6480       6490       6500       6510       6520       6530

        6390       6400       6410       6420       6430       6440
BH 10  ATGAGGATATAATCAGTTTATGGGATCAAAGCCTAAAGCCATGTGTAAAATTAACCCCAC
       : ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Licuw, AGGAGGATATAATCAGTTTATGGGATCAAAGCCTAAAGCCATGTGTAAAATTAACCCCAC
             6540       6550       6560       6570       6580       6590

        6450       6460       6470       6480       6490       6500
BH 10  TCTGTGTTAGTTTAAAGTGCACTGATTTGAAGAATGATACTAATACCAATAGTAGTAGCG
       ::::::::: :::::: ::::::::::::  ::: : ::::::::::::::::::::
Licuw, TCTGTGTTACTTTAAATTGCACTGATTTGGGGAAGGCTACTAATACCAATAGTAGTAATT
             6600       6610       6620       6630       6640       6650

        6510       6520       6530       6540       6550       6560
BH 10  GGAGA-ATGATAATGGAGAAAGGAGAGATAAAAAACTGCTCTTTCAATATCAGCACAAGC
       ::: : : :: :::    :::::::: :::::::::::::::::::::::: :::::::
Licuw, GGAAAGAAGA-AATA---AAAGGAGAAATAAAAAACTGCTCTTTCAATATCACCACAAGC
             6660          6670       6680       6690       6700
```

TABLE III-continued

(BH 10 v. LUCIW)
90.0% identity

```
         6570      6580      6590      6600      6610      6620
BH 10  ATAAGAGGTAAGGTGCAGAAAGAATATGCATTTTTTTATAAACTTGATATAATACCAATA
       ::::::: :::: : ::::::::: ::::: :::::  ::: :::::: :: ::::::::
Licuw, ATAAGAGATAAGATTCAGAAAGAAAATGCACTTTTTCGTAACCTTGATGTAGTACCAATA
       6710      6720      6730      6740      6750      6760

         6630           6640                6650      6660
BH 10  GATAATGATA------CTACCAGCTATAC---------GTTGACAAGTTGTAACACCTCA
       ::::::: ::      :::::: ::::::          ::::: :  ::::::::  :::
Licuw, GATAATGCTAGTACTACTACCAACTATACCAACTATAGGTTGATACATTGTAACAGATCA
       6770      6780      6790      6800      6810      6820

    6670      6680      6690      6700      6710      6720
BH 10  GTCATTACACAGGCCTGTCCAAAGGTATCCTTTGAGCCAATTCCCATACATTATTGTGCC
       :::::::::::::::::::::::::::: :::::::::::::::::::::::::::: ::
Licuw, GTCATTACACAGGCCTGTCCAAAGGTATCATTTGAGCCAATTCCCATACATTATTGTACC
       6830      6840      6850      6860      6870      6880

    6730      6740      6750      6760      6770      6780
BH 10  CCGGCTGGTTTTGCGATTCTAAAATGTAATAATAAGACGTTCAATGGAACAGGACCATGT
       :::::::::::::::::::::: :::::::::: :::::::::::: ::::::::::
Licuw, CCGGCTGGTTTTGCGATTCTAAAGTGTAATAATAAAACGTTCAATGGAAAAGGACCATGT
       6890      6900      6910      6920      6930      6940

    6790      6800      6810      6820      6830      6840
BH 10  ACAAATGTCAGCACAGTACAATGTACACATGGAATTAGGCCAGTAGTATCAACTCAACTG
       :::::::::::::::::::::::::::::::::::::::: :::: ::::::::::::
Licuw, ACAAATGTCAGCACAGTACAATGTACACATGGAATTAGGCCAATAGTGTCAACTCAACTG
       6950      6960      6970      6980      6990      7000

     6850      6860      6870      6880      6890      6900
BH 10  -CTGTTAAATGGCAGTCTAGCAGAAGAAGAGGTAGTAATTAGATCTGCCAATTTCACAGA
        ::::::::::::::::::::::::::::::::::::::::::: :::::::::  :
Licuw, TCTGTTAAATGGCAGTCTAGCAGAAGAAGAGGTAGTAATTAGATCTGACAATTTCACGAA
       7010      7020      7030      7040      7050      7060

     6910      6920      6930      6940      6950      6960
BH 10  CAATGCTAAAACCATAATAGTACAGCTGAACCAATCTGTAGAAATTAATTGTACAAGACC
       ::::::::::::::::::::::::::  ::::::::: :::::: ::::::::::
Licuw, CAATGCTAAAACCATAATAGTACAGCTGAATGAATCTGTAGCAATTAACTGTACAAGACC
       7070      7080      7090      7100      7110      7120

     6970      6980      6990      7000      7010      7020
BH 10  CAACAACAATACAAGAAAAAGTATCCGTATCCAGAGAGGACCAGGGAGAGCATTTGTTAC
       :::::::::::::::::::::::  :::      ::::::::::::::::::  :::
Licuw, CAACAACAATACAAGAAAAAGTATCTATAT------AGGACCAGGGAGAGCATTTCATAC
       7130      7140      7150            7160      7170      7180

     7030      7040         7050      7060      7070      7080
BH 10  AATAGGAAAAATA---GGAAATATGAGACAAGCACATTGTAACATTAGTAGAGCAAAATG
       :: ::::: ::::   ::: :::: ::: ::::::::::::::::::::::::: ::::
Licuw, AACAGGAAGAATAATAGGAGATATAAGAAAAGCACATTGTAACATTAGTAGAGCACAATG
             7190      7200      7210      7220      7230      7240

        7090      7100      7110      7120      7130      7140
BH 10  GAATAACACTTTAAAACAGATAGATAGCAAATTAAGAGAACAATTTGGAAATAATAAAAC
       :::::::::::: ::::::::: ::  :::::::::::::: ::::: ::::::::::
Licuw, GAATAACACTTTAGAACAGATAGTTAAAAAATTAAGAGAACAGTTTGGGAATAATAAAAC
             7250      7260      7270      7280      7290      7300

        7150      7160      7170      7180      7190      7200
BH 10  AATAATCTTTAAGCAGTCCTCAGGAGGGGACCCAGAAATTGTAACGCACAGTTTTAATTG
       :::: ::::::: :: ::::::::::::::::::::::::::: ::::::::::::::
Licuw, AATAGTCTTTAATCAATCCTCAGGAGGGGACCCAGAAATTGTAATGCACAGTTTTAATTG
             7310      7320      7330      7340      7350      7360

        7210      7220      7230      7240      7250        7260
BH 10  TGGAGGGGAATTTTTCTACTGTAATTCAACACAACTGTTTAATAGTACTTGGT--TTAAT
       : ::::::::::::::::::::::: :::::::::::::::: ::: :::   ::::
Licuw, TAGAGGGGAATTTTTCTACTGTAATACAACACAACTGTTTAATAATACATGGAGGTTAA-
             7370      7380      7390      7400      7410

          7270      7280      7290      7300      7310      7320
BH 10  AGTACTTGGAGTACTAAAGGGTCAAATAACACTGAAGGAAGTGACACAATCACCCTCCCA
       :  ::       ::: ::::          ::: :::::: ::::::::::  ::::::
Licuw, ATCAC-------ACTGAAGGA---------ACTAAAGGAAATGACACAATCATACTCCCA
    7420              7430              7440      7450      7460
```

TABLE III-continued

(BH 10 v. LUCIW)
90.0% identity

```
          7330       7340       7350       7360       7370       7380
BH 10   TGCAGAATAAAACAAATTATAAACATGTGGCAGGAAGTAGGAAAAGCAATGTATGCCCCT
        :: ::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Licuw,  TGTAGAATAAAACAAATTATAAACATGTGGCAGGAAGTAGGAAAAGCAATGTATGCCCCT
          7470       7480       7490       7500       7510       7520

          7390       7400       7410       7420       7430       7440
BH 10   CCCATCAGTGGACAAATTAGATGTTCATCAAATATTACAGGGCTGCTATTAACAAGAGAT
        :::::   : :::::::::::: ::::::::::::::::::::::::::::::::::::
Licuw,  CCCATTGGAGGACAAATTAGTTGTTCATCAAATATTACAGGGCTGCTATTAACAAGAGAT
          7530       7540       7550       7560       7570       7580

          7450          7460       7470       7480       7490       7500
BH 10   GGTGGTAATA--GCAAC-AATGAGTCCGAGATCTTCAGACCTGGAGGAGGAGATATGAGG
        :::::::   :   : ::: ::::::  ::::: ::::::::::::::::::::::::::
Licuw,  GGTGGTACAAATGTAACTAATGACACCGAGGTCTTCAGACCTGGAGGAGGAGATATGAGG
          7590       7600       7610       7620       7630       7640

              7510       7520       7530       7540       7550       7560
BH 10   GACAATTGGAGAAGTGAATTATATAAATATAAAGTAGTAAAAATTGAACCATTAGGAGTA
        :::::::::::::::::::::::::::::::::: :::::::::::::::::::: ::
Licuw,  GACAATTGGAGAAGTGAATTATATAAATATAAAGTAATAAAAATTGAACCATTAGGAATA
          7650       7660       7670       7680       7690       7700

              7570       7580       7590       7600       7610
BH 10   GCACCCACCAAGGCAAAGAGAAGAGTGGTGCAGAGAGAAAAAAGAGCAGTGGGAATAG--
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Licuw,  GCACCCACCAAGGCAAAGAGAAGAGTGGTGCAGAGAGAAAAAAGAGCAGTGGGAATAGTA
          7710       7720       7730       7740       7750       7760

        7620       7630       7640       7650       7660       7670
BH 10   -GAGCTTTGTTCCTTGGGTTCTTGGGAGCAGCAGGAAGCACTATGGGCGCAGCGTCAATG
         ::::: :::::::::::::::::::::::::::::::::: :::: :::: ::
Licuw,  GGAGCTATGTTCCTTGGGTTCTTGGGAGCAGCAGGAAGCACTATGGGGGCAGTGTCATTG
          7770       7780       7790       7800       7810       7820

        7680       7690       7700       7710       7720       7730
BH 10   ACGCTGACGGTACAGGCCAGACAATTATTGTCTGGTATAGTGCAGCAGCAGAACAATTTG
        :::::::::::::::::::::::::::::::::::::::::: ::::::::::::::
Licuw,  ACGCTGACGGTACAGGCCAGACAATTATTGTCTGGTATAGTGCAACAGCAGAACAATTTG
          7830       7840       7850       7860       7870       7880

        7740       7750       7760       7770       7780       7790
BH 10   CTGAGGGCTATTGAGGCGCAACAGCATCTGTTGCAACTCACAGTCTGGGGCATCAAGCAG
        :::::::::::::::::::::: ::::::::::::::::::::::::::::::::::::
Licuw,  CTGAGGGCTATTGAGGCGCAACAACATCTGTTGCAACTCACAGTCTGGGGCATCAAGCAG
          7890       7900       7910       7920       7930       7940

        7800       7810       7820       7830       7840       7850
BH 10   CTCCAGGCAAGAATCCTGGCTGTGGAAAGATACCTAAAGGATCAACAGCTCCTGGGGATT
        :::::::::::: :::::::::::::::::::::::: :::::::::::::: :  :::
Licuw,  CTCCAGGCAAGAGTCCTGGCTGTGGAAAGATACCTAAGGGATCAACAGCTCCTAG--ATT
           7950       7960       7970       7980       7990        8000

        7860       7870       7880       7890       7900       7910
BH 10   TGGGGTTGCTCTGGAAAACTCATTTGCACCACTGCTGTGCCTTGGAATGCTAGTTGGAGT
        :::::: :::::::::: ::::::::::::::::::::::::::::::::::::::::::
Licuw,  TGGGGT-GCTCTGGAAA-CTCATTTGCACCACTGCTGTGCCTTGGAATGCTAGTTGGAGT
              8010       8020       8030       8040       8050

        7920       7930       7940       7950       7960       7970
BH 10   AATAAATCTCTGGAACAGATTTGGAATAACATGACCTGGATGGAGTGGGACAGAGAAATT
        :::::::::::::::: : :::::: :::::::::::::: ::: ::::::: :::::::::
Licuw,  AATAAATCTCTGGAAGACATTTGGGATAACATGACCTG-ATGCAGTGGGAAAGAGAAATT
      8060       8070       8080       8090        8100       8110

        7980       7990       8000       8010       8020       8030
BH 10   AACAATTACACAAGCTTAATACACTCCTTAATTGAAGAATCGCAAAACCAGCAAGAAAAG
         :::::::::::: :  :::: :: ::::: :::::::::::::: ::::: :::::::::
Licuw,  GACAATTACACAAACACAATATACACCTTACTTGAAGAATCGCAGAACCAACAAGAAAAG
       8120       8130       8140       8150       8160       8170
```

TABLE III-continued

(BH 10 v. LUCIW)
90.0% identity

```
      8040      8050      8060      8070      8080      8090
BH 10  AATGAACAAGAATTATTGGAATTAGATAAATGGGCAAGTTTGTGGAATTGGTTTAACATA
       :::::::::::::::::: ::::: ::::: :::::::::::::::::::::::::: ::::
Licuw, AATGAACAAGAATTATTAGAATTGGATAAGTGGGCAAGTTTGTGGAATTGGTTTAGCATA
     8180      8190      8200      8210      8220      8230

      8100      8110      8120      8130      8140      8150
BH 10  ACAAATTGGCTGTGGTATATAAAATTATTCATAATGATAGTAGGAGGCTTGGTAGGTTTA
       ::::: ::::::::::::::::  ::::::::::::::::::::::::::::::::::
Licuw, ACAAACTGGCTGTGGTATATAAAGATATTCATAATGATAGTAGGAGGCTTGGTAGGTTTA
     8240      8250      8260      8270      8280      8290

      8160      8170      8180      8190      8200      8210
BH 10  AGAATAGTTTTTGCTGTACTTTCTGTAGTGAATAGAGTTAGGCAGGGATATTCACCATTA
       :::::::::::::::: :::::: ::::::::::::::::::::::: :::::::::
Licuw, AGAATAGTTTTTGCTGTGCTTTCTATAGTGAATAGAGTTAGGCAGGGATACTCACCATTG
     8300      8310      8320      8330      8340      8350

      8220      8230      8240      8250      8260      8270
BH 10  TCGTTTCAGACCCACCTCCCAATCCCGAGGGGACCCGACAGGCCCGAAGGAATAGAAGAA
       :: ::::::::::  :::::: : :::::   ::::::::: ::::: ::::: ::::::
Licuw, TCATTTCAGACCCGGCTCCCAGTGCCGAG---ACCCGACAG-CCCGACGGAATCGAAGAA
     8360      8370      8380          8390        8400      8410

      8280      8290      8300      8310      8320      8330
BH 10  GAAGGGGAGAGAGAGACAGAGACAGATCCATTCGATTAGTGAACGGATCCTTAGCACTTA
       :::::::::::::::::::::::::::: :::::::::: : :::: ::::::::::
Licuw, GAAGGGGAGAGAGAGACAGAGACAGATCCGTTCGATTAGTGGATGGATTCTTAGCACTTA
         8420      8430      8440      8450      8460      8470

      8340      8350      8360      8370      8380      8390
BH 10  TCTGGGACGATCTGCGGAGCCTGTGCCTCTTCAGCTACCACCGCTTGAGAGACTTACTCT
       ::::::: ::::::::::::::::::::::::::::  :: ::::::::::::::::
Licuw, TCTGGGAAGATCTGCGGAGCCTGTGCCTCTTCAGCTACCGGCGGTTGAGAGACTTACTCT
         8480      8490      8500      8510      8520      8530

      8400      8410      8420      8430      8440      8450
BH 10  TGATTGTAACGAGGATTGTGGAACTTCTGGGACGCAGGGGGTGGGAAGCCCTCAAATATT
       :::::: : :::::: ::::::: ::::::: : ::::::::::::   ::::::::::
Licuw, TGATTGCAGCGAGGACTGTGGAAATTCTGGGGCACAGGGGGTGGGAA---CTCAAATATT
         8540      8550      8560      8570      8580          8590

      8460      8470      8480      8490      8500      8510
BH 10  GGTGGAATCTCCTACAGTATTGGAGTCAGGAGCTAAAGAATAGTGCTGTTAGCTTGCTCA
       :::::: :::::: :::::::::: :::::: ::::::::::::::::::::: :::::
Licuw, GGTGGAGTCTCCTGCAGTATTGGATTCAGGAACTAAAGAATAGTGCTGTTAGCTGGCTCA
            8600      8610      8620      8630      8640      8650

      8520      8530      8540      8550      8560      8570
BH 10  ATGCCACAGCTATAGCAGTAGCTGAGGGGACAGATAGGGTTATAGAAGTAGTACAAGGAG
       : ::::::::::::::::: :::::::::::::::::::::::::::: :::: :::
Licuw, ACGCCACAGCTATAGCAGTAACTGAGGGGACAGATAGGGTTATAGAAGTAGCACAAAGAG
            8660      8670      8680      8690      8700      8710

      8580      8590      8600      8610      8620      8630
BH 10  CTTATAGAGCTATTCGCCACATACCTAGAAGAATAAGACAGGGCTTGGAAAGGATTTTGC
       :::::::::::::: :::::::: ::::::::: :::::   :::::::::: ::::::
Licuw, CTTATAGAGCTATTCTCCACATACATAGAAGAATTAGACA---CTTGGAAAGGCTTTTGC
            8720      8730      8740      8750          8760

      8640      8650      8660      8670      8680      8690
BH 10  TATAAGATGGGTGGCAAGTGGTCAAAAAGTAGTGTGGTTGGATGGCCTGCTGTAAGGGAA
       :::::::::::  :   :::::::::::  : ::: :::  :::::: ::::: ::::::::
Licuw, TATAAGATGGGGG---AGTGGTCAAAACG-AGTATGGG-GGATGGTCTGCTATAAGGGAA
     8770      8780          8790        8800        8810      8820

      8700      8710                    8720      8730      8740
BH 10  AGAATGAGACGAGCTGAGCCA-----------GCAGCAGATGGGGTGGGAGCAGCATCT
       :::::::::::::::::::::            :::::::::::: ::::: ::: ::::
Licuw, AGAATGAGACGAGCTGAGCCACGAGCTGAGCCAGCAGCAGATGGG-TGGGA-CAGTATCT
          8830      8840      8850      8860        8870        8880

        8750      8760      8770      8780      8790      8800
BH 10  CGAGACCTAGAAAAACATGGAGCAATCACAAGTAGCAACACAGCAGCTAACAATGCTGAT
       :::::::: ::::::::::::  :::::::::::::: ::::::::::  :::::::::
Licuw, CGAGACCTGGAAAAACATGGA--AATCACAAGTAGCAATACAGCAGCTACTAATGCTGAT
            8890      8900        8910      8920      8930
```

TABLE III-continued

(BH 10 v. LUCIW)
90.0% identity

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        8810      8820      8830      8840      8850      8860
BH 10  TGTGCCTGGCTAGAAGCACAAGAGGAGGAGGAGGTGGGTTTTCCAGTCACACCTCAGGTA
       :::::::::::::::::::::::::::: :::::::::::::::::: ::::::::::
Licuw, TGTGCCTGGCTAGAAGCACAAGAGGAGGAAGAGGTGGGTTTTCCAGTCAGACCTCAGGTA
    8940      8950      8960      8970      8980      8990

        8870      8880      8890      8900      8910      8920
BH 10  CCTTTAAGACCAATGACTTACAAGGCAGCTGTAGATCTTAGCCACTTTTTAAAAGAAAAG
       :::::::::::::::::::::::::::: ::::: ::::::::::::::::::::::
Licuw, CCTTTAAGACCAATGACTTACAAGGCAGCTTTAGATATTAGCCACTTTTTAAAAGAAAAG
    9000      9010      9020      9030      9040      9050

        8930      8940      8950      8960      8970      8980
BH 10  GGGGGACTGGAAGGGCTAATTCACTCCCAACGAAGACAAGATATCCTTGATCTGTGGATC
       ::::::::::::::::::::   :::::: :::::::::: ::::::::::::::::::
Licuw, GGGGGACTGGAAGGGCTAATTTGGTCCCAAAGAAGACAAGAGATCCTTGATCTGTGGATC
    9060      9070      9080      9090      9100      9110

        8990      9000      9010      9020      9030      9040
BH 10  TACCACACACAAGGCTACTTCCCTGATTAGCAGAACTACACACCAGGGCCAGGGATCAGA
       :::::::::::::::::::::::::::: :::::: ::::::::::::::::::::::
Licuw, TACCACACACAAGGCTACTTCCCTGATTGGCAGAATTACACACCAGGGCCAGGGATCAGA
    9120      9130      9140      9150      9160      9170

        9050      9060      9070      9080      9090      9100
BH 10  TATCCACTGACCTTTGGATGGTGCTACAAGCTAGTACCAGTTGAGCCAGAGAAGTTAGAA
       :::::::::::::::::::::::: :::::::::::::::::::::::::::: :::::
Licuw, TATCCACTGACCTTTGGATGGTGCTTCAAGCTAGTACCAGTTGAGCCAGAGAAGGTAGAA
    9180      9190      9200      9210      9220      9230

        9110      9120      9130      9140      9150      9160
BH 10  GAAGCCAACAAAGGAGAGAACACCAGCTTGTTACACCCTGTGAGCCTGCATGGAATGGAT
       :: :::::  :::::::::::::  :::::::::::::::: :::::::::::: :::::
Licuw, GAGGCCAATGAAGGAGAGAACAA-AGCTTGTTACACCCTATGAGCCTGCATGGGATGGAG
    9240      9250      9260       9270      9280      9290

        9170      9180      9190      9200      9210      9220
BH 10  GACCCGGAGAGAGAAGTGTTAGAGTGGAGGTTTGACAGCCGCCTAGCATTTCATCACATG
       ::: :::::: :::::::::: ::::::::::::::::   ::::::::::::::::::
Licuw, GACGCGGAGAAAGAAGTGTTAGTGTGGAGGTTTGACAGCAAACTAGCATTTCATCACATG
     9300      9310      9320      9330      9340      9350

        9230      9240      9250      9260      9270      9280
BH 10  GCCCGAGAGCTGCATCCGGAGTACTTCAAGAACTGCTGACATCGAGCTTGCTACAAGGGA
       :::::::::::::::::::::::: :::  :::::::::::::::::: ::::::::::
Licuw, GCCCGAGAGCTGCATCCGGAGTACTACAAAGACTGCTGACATCGAGCTTTCTACAAGGGA
     9360      9370      9380      9390      9400      9410

        9290      9300       9310      9320      9330      9340
BH 10  CTTTCCGCTGGGGACTTTCCAGG-AGGCGTGGCCTGGGCGGGACTGGGGAGTGGCGAGCC
       :::::::::::::::::::::: ::::::::::::::::::::::::::::::  ::
Licuw, CTTTCCGCTGGGGACTTTCCAGGGAGGCGTGGCCTGGGCGGGACTGGGGAGTGGCGT-CC
     9420      9430      9440      9450      9460      9470

         9350      9360      9370      9380      9390      9400
BH 10  CTCAGATCCTGCATATAAGGAGCTGCTTTTTGCCTGTACTGGGTCTCTCTGGTTAGACCA
       ::::::: :::::::::::: :::::::::::::::::::::::::::::::::::::::
Licuw, CTCAGATGCTGCATATAAGCAGCTGCTTTTTGCCTGTACTGGGTCTCTCTGGTTAGACCA
      9480      9490      9500      9510      9520      9530

         9410      9420
BH 10  GATCTGAGCCTGGGAGCTC----------------------------------------
       ::::::::::::::::::
Licuw, GATCTGAGCCTGGGAGCTCTCTGGCTAACTAGGGAACCCACTGCTTAAGCCTCAATAAAG
      9540      9550      9560      9570      9580      9590

BH 10  ------------------------------------------------------------

Licuw, CTTGCCTTGAGTGCTTCAAGTAGTGTGTGCCCGTCTGTTGTGTGACTCTGGTAACTAGAG
      9600      9610      9620      9630      9640      9650

BH 10  -------------------------------------------

Licuw, ATCCCTCAGACCCTTTTAGTCAGTGTGGAAAAATCTCTAGCAG
      9660      9670      9680      9690      9700
```

What we claim is:

1. A composition comprising a duplex formed between a Human Immunodeficiency Virus Type-1 (HIV-1) nucleic acid and a single-stranded nucleic acid of at least 18 contiguous nucleotides comprising a nucleotide sequence selected from the group consisting of:

(i) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_2 having ATCC Accession No. 40231;

(ii) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_3 having ATCC Accession No. 40232;

(iii) a nucleotide sequence of either strand of viral DNA from clone BH10 having ATCC Accession No. 40125;

(iv) a nucleotide sequence of either strand of viral DNA from clone BH5 having ATCC Accession No. 40126;

(v) a nucleotide sequence of either strand of viral DNA from clone BH8 having ATCC Accession No. 40127;

(vi) a nucleotide sequence of either strand of viral DNA from clone pHXB3 having ATCC Accession No. 67081;

(vii) a nucleotide sequence of either strand of viral DNA from clone pHXB-2D having ATCC Accession No. 67082;

(viii) a nucleotide sequence of either strand of viral DNA from *E. coli* clone X10-1 having ATCC Accession No. 67083; and

(ix) an HIV-1 nucleotide sequence from the H9/HTLV-III cell line having ATCC Accession No. CRL 8543;

wherein the single-stranded nucleic acid does not form a duplex with HTLV-I and HTLV-II nucleic acids under conditions of stringency for hybridization under which the single-stranded nucleic acid forms a duplex with the HIV-1 nucleic acid;

wherein the duplex is outside of a mammalian cell and outside of an HIV-1 particle;

wherein the duplex comprises a double-stranded region of at least 18 contiguous nucleotides and a single-stranded region on either side of the double-stranded region that is longer than the double-stranded region; and

wherein the single-stranded nucleic acid comprises a label.

2. The composition of claim **1**, wherein the single-stranded nucleic acid comprises a nucleotide sequence which is part of an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or part of an HIV-1 long terminal repeat region.

3. The composition of claim **1**, wherein the single-stranded nucleic acid is selected from the group consisting of:

(i) a single-stranded nucleic acid consisting of from 18 to 103 nucleotides comprising a nucleotide sequence of at least 18 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 env open reading frame, an HIV-1 pol open reading frame or from an HIV-1 long terminal repeat region;

(ii) a single-stranded nucleic acid consisting of from 32 to 103 nucleotides comprising a nucleotide sequence of at least 32 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 env open reading frame, an HIV-1 pol open reading frame or from an HIV-1 long terminal repeat region;

(iii) a single-stranded nucleic acid consisting of from 20 to 100 nucleotides comprising a nucleotide sequence of at least 20 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 env open reading frame, an HIV-1 pol open reading frame or from an HIV-1 long terminal repeat region;

(iv) a single-stranded nucleic acid comprising a nucleotide sequence of at least about 32 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 env open reading frame, an HIV-1 pol open reading frame or from an HIV-1 long terminal repeat region; and

(v) a single-stranded nucleic acid comprising a nucleotide sequence of at least about 20 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 env open reading frame, an HIV-1 pol open reading frame or from an HIV-1 long terminal repeat region.

4. The composition of claim **1**, wherein the duplex is bound to a solid support.

5. The composition of claim **1**, wherein the single-stranded nucleic acid is randomly generated from an HIV-1 nucleic acid.

6. The composition of claim **1**, wherein the single-stranded nucleic acid comprises DNA.

7. The composition of claim **1**, wherein the single-stranded nucleic acid comprises RNA.

8. The composition of claim **1**, wherein single-stranded nucleic acid is a cDNA.

9. The composition of claim **1**, wherein the label is attached to the single-stranded nucleic acid and wherein the label is not an additional nucleic acid.

10. The composition of claim **1**, wherein the single-stranded nucleic acid comprises a non-HIV-1 nucleotide sequence.

11. The composition of claim **1**, wherein the single-stranded nucleic acid is chemically made at least in part.

12. The composition of claim **1**, wherein the HIV-1 nucleic acid is a full-length HIV-1 nucleic acid.

13. The composition of claim **1**, wherein the HIV-1 nucleic acid is not a full-length HIV-1 nucleic acid.

14. A method for preparing a DNA construct specific for Human Immunodeficiency Virus Type-1 (HIV-1) comprising the step of inserting into a vector a nucleic acid of at least 18 contiguous nucleotides comprising a nucleotide sequence selected from the group consisting of

(i) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_2 having ATCC Accession No. 40231;

(ii) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_3 having ATCC Accession No. 40232;

(iii) a nucleotide sequence of either strand of viral DNA from clone BH10 having ATCC Accession No. 40125;

(iv) a nucleotide sequence of either strand of viral DNA from clone BH5 having ATCC Accession No. 40126;

(v) a nucleotide sequence of either strand of viral DNA from clone BH8 having ATCC Accession No. 40127;

(vi) a nucleotide sequence of either strand of viral DNA from clone pHXB3 having ATCC Accession No. 67081;

(vii) a nucleotide sequence of either strand of viral DNA from clone pHXB-2D having ATCC Accession No. 67082;

(viii) a nucleotide sequence of either strand of viral DNA from *E. coli* clone X10-1 having ATCC Accession No. 67083; and

(ix) an HIV-1 nucleotide sequence from the H9/HTLV-III cell line having ATCC Accession No. CRL 8543;

whereby a DNA construct comprising an inserted nucleic acid is obtained.

15. The method according to claim **14**, wherein the DNA construct permits making an RNA transcript of the inserted nucleic acid.

16. A method for replicating DNA specific for HIV-1 comprising the step of growing a cell containing the DNA construct of claim **14** under conditions whereby the inserted nucleic acid is replicated.

17. A method for producing a recombinant HIV-1 polypeptide comprising the step of growing a cell containing the DNA construct of claim **14** under conditions whereby the inserted nucleic acid is expressed to allow production of the recombinant HIV-1 polypeptide in the cell.

18. A nucleic acid of at least 18 contiguous nucleotides comprising a nucleotide sequence selected from the group consisting of

(i) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_2 having ATCC Accession No. 40231;

(ii) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_3 having ATCC Accession No. 40232;

(iii) a nucleotide sequence of either strand of viral DNA from clone BH10 having ATCC Accession No. 40125;

(iv) a nucleotide sequence of either strand of viral DNA from clone BH5 having ATCC Accession No. 40126;

(v) a nucleotide sequence of either strand of viral DNA from clone BH8 having ATCC Accession No. 40127;

(vi) a nucleotide sequence of either strand of viral DNA from clone pHXB3 having ATCC Accession No. 67081;

(vii) a nucleotide sequence of either strand of viral DNA from clone pHXB-2D having ATCC Accession No. 67082;

(viii) a nucleotide sequence of either strand of viral DNA from *E. coli* clone X10-1 having ATCC Accession No. 67083; and

(ix) a Human Immunodeficiency Virus Type-1 (HIV-1) nucleotide sequence from the H9/HTLV-III cell line having ATCC Accession No. CRL 8543;

wherein the nucleic acid does not form a duplex with HTLV-I and HTLV-II nucleic acids under conditions of stringency for hybridization under which the nucleic acid forms a duplex with an HIV-1 nucleic acid; and

wherein the nucleic acid is covalently attached to a solid support.

19. The nucleic acid of claim **18**, wherein the nucleic acid comprises a nucleotide sequence which is part of an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or part of an HIV-1 long terminal repeat region.

20. The nucleic acid of claim **18**, wherein the nucleic acid is selected from the group consisting of

(i) a nucleic acid consisting of from 18 to 103 nucleotides comprising a nucleotide sequence of at least 18 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region;

(ii) a nucleic acid consisting of from 32 to 103 nucleotides comprising a sequence of at least 32 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region;

(iii) a nucleic acid consisting of from 20 to 100 nucleotides comprising a sequence of at least 20 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region;

(iv) a nucleic acid comprising a sequence of at least about 32 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region; and

(v) a nucleic acid comprising a sequence of at least about 20 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region.

21. The nucleic acid of claim **18**, wherein the nucleic acid is a restriction fragment from an HIV-1 nucleic acid.

22. The nucleic acid of claim **18**, wherein the nucleic acid is randomly generated from an HIV-1 nucleic acid.

23. The nucleic acid of claim **18**, wherein the nucleic acid comprises DNA.

24. The nucleic acid of claim **18**, wherein the nucleic acid comprises RNA.

25. The nucleic acid of claim **18**, wherein the nucleic acid is a cDNA.

26. The nucleic acid of claim **18**, wherein the nucleic acid comprises a label.

27. The nucleic acid of claim **18**, wherein the nucleic acid comprises a non-HIV-1 nucleotide sequence.

28. The nucleic acid of claim **18**, wherein the nucleic acid is chemically made at least in part.

29. The nucleic acid of claim **18**, wherein the nucleic acid is a double-stranded nucleic acid.

30. The nucleic acid of claim **18**, wherein the nucleic acid is a single-stranded nucleic acid.

31. A single-stranded nucleic acid of at least 18 contiguous nucleotides comprising a nucleotide sequence selected from the group consisting of

(i) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_2 having ATCC Accession No. 40231;

(ii) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_3 having ATCC Accession No. 40232;

(iii) a nucleotide sequence of either strand of viral DNA from clone BH10 having ATCC Accession No. 40125;

(iv) a nucleotide sequence of either strand of viral DNA from clone BH5 having ATCC Accession No. 40126;

(v) a nucleotide sequence of either strand of viral DNA from clone BH8 having ATCC Accession No. 40127;

(vi) a nucleotide sequence of either strand of viral DNA from clone pHXB3 having ATCC Accession No. 67081;

(vii) a nucleotide sequence of either strand of viral DNA from clone pHXB-2D having ATCC Accession No. 67082;

(viii) a nucleotide sequence of either strand of viral DNA from *E. coli* clone X10-1 having ATCC Accession No. 67083; and

(ix) a Human Immunodeficiency Virus Type-1 (HIV-1) nucleotide sequence from the H9/HTLV-III cell line having ATCC Accession No. CRL 8543;

wherein the single-stranded nucleic acid does not form a duplex with HTLV-I and HTLV-II nucleic acids under conditions of stringency for hybridization under which the single-stranded nucleic acid forms a duplex with an HIV-1 nucleic acid;

wherein the single-stranded nucleic acid is within a duplex comprising the HIV-1 nucleic acid; and

wherein the duplex is covalently attached to a solid support.

32. The single-stranded nucleic acid of claim **31**, wherein the single-stranded nucleic acid is complementary to a sequence which is part of an HIV-1 gag open reading frame,

an HIV-1 pol open reading frame, an HIV-1 env open reading frame or part of an HIV-1 long terminal repeat region.

33. The single-stranded nucleic acid of claim **31**, wherein the single-stranded nucleic acid is selected from the group consisting of

(i) a single-stranded nucleic acid consisting of from 18 to 103 nucleotides comprising a sequence of at least 18 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region;

(ii) a single-stranded nucleic acid consisting of from 32 to 103 nucleotides comprising a sequence of at least 32 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region;

(iii) a single-stranded nucleic acid consisting of from 20 to 100 nucleotides comprising a sequence of at least 20 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region;

(iv) a single-stranded nucleic acid comprising a sequence of at least about 32 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region; and

(v) a single-stranded nucleic acid comprising a sequence of at least about 20 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region.

34. The single-stranded nucleic acid of claim **31**, wherein the HIV-1 nucleic acid is bound to a solid support.

35. The single-stranded nucleic acid of claim **31**, wherein the single-stranded nucleic acid is randomly generated from an HIV-1 nucleic acid.

36. The single-stranded nucleic acid of claim **31**, wherein the single-stranded nucleic acid comprises DNA.

37. The single-stranded nucleic acid of claim **31**, wherein the single-stranded nucleic acid comprises RNA.

38. The single-stranded nucleic acid of claim **31**, wherein the single-stranded nucleic acid is a cDNA.

39. The single-stranded nucleic acid of claim **31**, wherein the single-stranded nucleic acid comprises a label.

40. The single-stranded nucleic acid of claim **31**, wherein the single-stranded nucleic acid comprises a non-HIV-1 nucleotide sequence.

41. The single-stranded nucleic acid of claim **31**, wherein the single-stranded nucleic acid is chemically made at least in part.

42. The single-stranded nucleic acid of claim **31**, wherein the HIV-1 nucleic acid is a full-length HIV-1 nucleic acid.

43. The single-stranded nucleic acid of claim **31**, wherein the HIV-1 nucleic acid is not a full-length HIV-1 nucleic acid.

44. A nucleic acid of at least 18 contiguous nucleotides comprising a nucleotide sequence selected from the group consisting of

(i) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_2 having ATCC Accession No. 40231;

(ii) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_3 having ATCC Accession No. 40232;

(iii) a nucleotide sequence of either strand of viral DNA from clone BH10 having ATCC Accession No. 40125;

(iv) a nucleotide sequence of either strand of viral DNA from clone BH5 having ATCC Accession No. 40126;

(v) a nucleotide sequence of either strand of viral DNA from clone BH8 having ATCC Accession No. 40127;

(vi) a nucleotide sequence of either strand of viral DNA from clone pHXB3 having ATCC Accession No. 67081;

(vii) a nucleotide sequence of either strand of viral DNA from clone pHXB-2D having ATCC Accession No. 67082;

(viii) a nucleotide sequence of either strand of viral DNA from *E. coli* clone X10-1 having ATCC Accession No. 67083; and

(ix) a Human Immunodeficiency Virus Type-1 (HIV-1) nucleotide sequence from the H9/HTLV-III cell line having ATCC Accession No. CRL 8543;

wherein the nucleic acid does not form a duplex with HTLV-I and HTLV-II nucleic acids under conditions of stringency for hybridization under which the nucleic acid forms a duplex with an HIV-1 nucleic acid;

wherein the nucleic acid comprises a detectable label covalently attached to the nucleic acid; and

wherein the detectable label is not an additional nucleic acid.

45. The nucleic acid of claim **44**, wherein the nucleic acid comprises a nucleotide sequence which is part of an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or part of an HIV-1 long terminal repeat region.

46. The nucleic acid of claim **44**, wherein the nucleic acid is selected from the group consisting of

(i) a nucleic acid consisting of from 18 to 103 nucleotides comprising a sequence of at least 18 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region;

(ii) a nucleic acid consisting of from 32 to 103 nucleotides comprising a sequence of at least 32 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region;

(iii) a nucleic acid consisting of from 20 to 100 nucleotides comprising a sequence of at least 20 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region;

(iv) a nucleic acid comprising a sequence of at least about 32 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region n; and

(v) a nucleic acid comprising a sequence of at least about 20 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region.

47. The nucleic acid of claim **44**, wherein the nucleic acid is a restriction fragment from an HIV-1 nucleic acid.

48. The nucleic acid of claim **44**, wherein the nucleic acid is randomly generated from an HIV-1 nucleic acid.

49. The nucleic acid of claim **44**, wherein the nucleic acid comprises DNA.

50. The nucleic acid of claim **44**, wherein the nucleic acid comprises RNA.

51. The nucleic acid of claim **44**, wherein the nucleic acid is a cDNA.

52. The nucleic acid of claim **44**, wherein the nucleic acid comprises a non-HIV-1 nucleotide sequence.

53. The nucleic acid of claim **44**, wherein the nucleic acid is chemically made at least in part.

54. The nucleic acid of claim **44**, wherein the nucleic acid is a double-stranded nucleic acid.

55. The nucleic acid of claim **44**, wherein the nucleic acid is a single-stranded nucleic acid.

56. A nucleic acid of at least 18 contiguous nucleotides comprising a nucleotide sequence selected from the group consisting of

(i) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_2 having ATCC Accession No. 40231;

(ii) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_3 having ATCC Accession No. 40232;

(iii) a nucleotide sequence of either strand of viral DNA from clone BH10 having ATCC Accession No. 40125;

(iv) a nucleotide sequence of either strand of viral DNA from clone BH5 having ATCC Accession No. 40126;

(v) a nucleotide sequence of either strand of viral DNA from clone BH8 having ATCC Accession No. 40127;

(vi) a nucleotide sequence of either strand of viral DNA from clone pHXB3 having ATCC Accession No. 67081;

(vii) a nucleotide sequence of either strand of viral DNA from clone pHXB-2D having ATCC Accession No. 67082;

(viii) a nucleotide sequence of either strand of viral DNA from *E. coli* clone X10-1 having ATCC Accession No. 67083; and

(ix) a Human Immunodeficiency Virus Type-1 (HIV-1) nucleotide sequence from the H9/HTLV-III cell line having ATCC Accession No. CRL 8543;

wherein the nucleic acid does not form a duplex with HTLV-I and HTLV-II nucleic acids under conditions of stringency for hybridization under which the nucleic acid forms a duplex with an HIV-1 nucleic acid;

wherein the nucleic acid is outside of a mammalian cell and outside of a viral particle; and

wherein the nucleic acid is attached to a non-HIV-1 nucleic acid through a covalent bond.

57. The nucleic acid of claim **56**, wherein the nucleic acid is complementary to a sequence which is part of an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or part of an HIV-1 long terminal repeat region.

58. The nucleic acid of claim **56**, wherein the nucleic acid is selected from the group consisting of

(i) a nucleic acid consisting of from 18 to 103 nucleotides comprising a sequence of at least 18 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region;

(ii) a nucleic acid consisting of from 32 to 103 nucleotides comprising a sequence of at least 32 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region;

(iii) a nucleic acid consisting of from 20 to 100 nucleotides comprising a sequence of at least 20 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region;

(iv) a nucleic acid comprising a sequence of at least about 32 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region; and

(v) a nucleic acid comprising a sequence of at least about 20 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region.

59. The nucleic acid of claim **56**, wherein the nucleic acid is a restriction fragment from an HIV-1 nucleic acid.

60. The nucleic acid of claim **56**, wherein the nucleic acid is randomly generated from an HIV-1 nucleic acid.

61. The nucleic acid of claim **56**, wherein the nucleic acid comprises DNA.

62. The nucleic acid of claim **56**, wherein the nucleic acid comprises RNA.

63. The nucleic acid of claim **56**, wherein the nucleic acid is a cDNA.

64. The nucleic acid of claim **56**, wherein the nucleic acid comprises a label.

65. The nucleic acid of claim **56**, wherein the nucleic acid is chemically made at least in part.

66. The nucleic acid of claim **56**, wherein the nucleic acid is a double-stranded nucleic acid.

67. The nucleic acid of claim **56**, wherein the nucleic acid is a single-stranded nucleic acid.

68. A composition comprising a duplex formed between:

(A) a single-stranded nucleic acid of between 18 and 103 contiguous nucleotides and comprising a nucleotide sequence selected from the group consisting of:

(i) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_2 having ATCC Accession No. 40231;

(ii) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_3 having ATCC Accession No. 40232;

(iii) a nucleotide sequence of either strand of viral DNA from clone BH10 having ATCC Accession No. 40125;

(iv) a nucleotide sequence of either strand of viral DNA from clone BH5 having ATCC Accession No. 40126;

(v) a nucleotide sequence of either strand of viral DNA from clone BH8 having ATCC Accession No. 40127;

(vi) a nucleotide sequence of either strand of viral DNA from clone pHXB3 having ATCC Accession No. 67081;

(vii) a nucleotide sequence of either strand of viral DNA from clone pHXB-2D having ATCC Accession No. 67082;

(viii) a nucleotide sequence of either strand of viral DNA from *E. coli* clone X10-1 having ATCC Accession No. 67083; and

(ix) a Human Immunodeficiency Virus Type-1 (HIV-1) nucleotide sequence from the H9/HTLV-III cell line having ATCC Accession No. CRL 8543; and

(B) an HIV-1 nucleic acid selected from the group consisting of:

(a) an HIV-1 nucleic acid comprising a nucleotide sequence encoding a full-length gag polypeptide or its complement;

(b) an HIV-1 nucleic acid comprising a nucleotide sequence encoding a full-length pol polypeptide or its complement;

(c) an HIV-1 nucleic acid comprising a nucleotide sequence encoding a full-length env polypeptide or its complement; and

(d) an HIV-1 nucleic acid comprising a nucleotide sequence for a long terminal repeat region comprising R and U_3 regions or their complements;

wherein the single-stranded nucleic acid of (A) does not form a duplex with HTLV-I and HTLV-II nucleic acids

under conditions of stringency for hybridization under which the nucleic acid of (A) forms a duplex with the HIV-1 nucleic acid of (B);

wherein the duplex is outside of a mammalian cell and outside of a viral particle;

wherein the duplex comprises a double-stranded region of between 18 and 103 contiguous nucleotides and a single-stranded region on either side of the double-stranded region that is longer than the double-stranded region; and

wherein the single-stranded nucleic acid comprises a label.

69. The composition of claim **68**, wherein the single-stranded nucleic acid comprises a nucleotide sequence which is part of an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or part of an HIV-1 long terminal repeat region.

70. The composition of claim **68**, wherein the single-stranded nucleic acid is selected from the group consisting of

(i) a single-stranded nucleic acid consisting of from 18 to 103 nucleotides comprising a sequence of at least 18 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region;

(ii) a single-stranded nucleic acid consisting of from 32 to 103 nucleotides comprising a sequence of at least 32 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region;

(iii) a single-stranded nucleic acid consisting of from 20 to 100 nucleotides comprising a sequence of at least 20 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region;

(iv) a single-stranded nucleic acid comprising a sequence of at least about 32 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region; and

(v) a single-stranded nucleic acid comprising a sequence of at least about 20 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region.

71. The composition of claim **68**, wherein the single-stranded nucleic acid is randomly generated from an HIV-1 nucleic acid.

72. The composition of claim **68**, wherein the single-stranded nucleic acid comprises DNA.

73. The composition of claim **68**, wherein the single-stranded nucleic acid comprises RNA.

74. The composition of claim **68**, wherein the single-stranded nucleic acid is a cDNA.

75. The composition of claim **68**, wherein the label is attached to the single-stranded nucleic acid and wherein the label is not an additional nucleic acid.

76. The composition of claim **68**, wherein the single-stranded nucleic acid comprises a non-HIV-1 nucleotide sequence.

77. The composition of claim **68**, wherein the single-stranded nucleic acid is chemically made at least in part.

78. The composition of claim **68**, wherein the single-stranded nucleic acid is bound to a solid support.

79. The composition of claim **68**, wherein the duplex is bound to a solid support.

80. The composition of claim **68**, wherein the HIV-1 nucleic acid is a full-length HIV-1 nucleic acid.

81. The composition of claim **68**, wherein the HIV-1 nucleic acid is not a full-length HIV-1 nucleic acid.

82. A composition comprising:

(A) a duplex; and

(B) a compound selected from the group consisting of sodium saline citrate, formamide, and dextran sulfate;

wherein the duplex comprises a Human Immunodeficiency Virus Type-1 (HIV-1) nucleic acid having a length of at least 300 nucleotides hybridized to a single-stranded nucleic acid of between 18 and 103 contiguous nucleotides and comprising a nucleotide sequence selected from the group consisting of:

(i) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_2 having ATCC Accession No. 40231;

(ii) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_3 having ATCC Accession No. 40232;

(iii) a nucleotide sequence of either strand of viral DNA from clone BH10 having ATCC Accession No. 40125;

(iv) a nucleotide sequence of either strand of viral DNA from clone BH5 having ATCC Accession No. 40126;

(v) a nucleotide sequence of either strand of viral DNA from clone BH8 having ATCC Accession No. 40127;

(vi) a nucleotide sequence of either strand of viral DNA from clone pHXB3 having ATCC Accession No. 67081;

(vii) a nucleotide sequence of either strand of viral DNA from clone pHXB-2D having ATCC Accession No. 67082;

(viii) a nucleotide sequence of either strand of viral DNA from *E. coli* clone X10-1 having ATCC Accession No. 67083; and

(ix) a Human Immunodeficiency Virus Type-1 (HIV-1) nucleotide sequence from the H9/HTLV-III cell line having ATCC Accession No. CRL 8543;

wherein the single-stranded nucleic acid does not form a duplex with HTLV-I and HTLV-II nucleic acids under conditions of stringency for hybridization under which the single-stranded nucleic acid forms a duplex with the HIV-1 nucleic acid; and

wherein the duplex comprises a double-stranded region and a single-stranded region that is longer than the double-stranded region.

83. The composition of claim **82**, wherein the single-stranded nucleic acid comprises a sequence which is part of an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or part of an HIV-1 long terminal repeat region.

84. The composition of claim **82**, wherein the single-stranded nucleic acid is selected from the group consisting of

(i) a single-stranded nucleic acid consisting of from 18 to 103 nucleotides comprising a sequence of at least 18 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region;

(ii) a single-stranded nucleic acid consisting of from 32 to 103 nucleotides comprising a sequence of at least 32 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region;

(iii) a single-stranded nucleic acid consisting of from 20 to 100 nucleotides comprising a sequence of at least 20 contiguous nucleotides from an HIV-1 gag open reading

frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region;

(iv) a single-stranded nucleic acid comprising a sequence of at least about 32 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region; and

(v) a single-stranded nucleic acid comprising a sequence of at least about 20 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region.

85. The composition of claim **82**, wherein the single-stranded nucleic acid is randomly generated from an HIV-1 nucleic acid.

86. The composition of claim **82**, wherein the single-stranded nucleic acid comprises DNA.

87. The composition of claim **82**, wherein the single-stranded nucleic acid comprises RNA.

88. The composition of claim **82**, wherein the single-stranded nucleic acid is a cDNA.

89. The composition of claim **82**, wherein the single-stranded nucleic acid comprises a label.

90. The composition of claim **82**, wherein the single-stranded nucleic acid comprises a non-HIV-1 nucleotide sequence.

91. The composition of claim **82**, wherein the single-stranded nucleic acid is chemically made at least in part.

92. The composition of claim **82**, wherein the single-stranded nucleic acid is bound to a solid support.

93. The composition of claim **82**, wherein the duplex is bound to a solid support.

94. The composition of claim **82**, wherein the HIV-1 nucleic acid is a full-length HIV-1 nucleic acid.

95. The composition of claim **82**, wherein the HIV-1 nucleic acid is not a full-length HIV-1 nucleic acid.

96. A composition comprising a duplex formed between a Human Immunodeficiency Virus Type-1 (HIV-1) nucleic acid and a single-stranded nucleic acid of at least 18 contiguous nucleotides and comprising a nucleotide sequence selected from the group consisting of:

(i) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_2 having ATCC Accession No. 40231;

(ii) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_3 having ATCC Accession No. 40232;

(iii) a nucleotide sequence of either strand of viral DNA from clone BH10 having ATCC Accession No. 40125;

(iv) a nucleotide sequence of either strand of viral DNA from clone BH5 having ATCC Accession No. 40126;

(v) a nucleotide sequence of either strand of viral DNA from clone BH8 having ATCC Accession No. 40127;

(vi) a nucleotide sequence of either strand of viral DNA from clone pHXB3 having ATCC Accession No. 67081;

(vii) a nucleotide sequence of either strand of viral DNA from clone pHXB-2D having ATCC Accession No. 67082;

(viii) a nucleotide sequence of either strand of viral DNA from *E. coli* clone X10-1 having ATCC Accession No. 67083; and

(ix) an HIV-1 nucleotide sequence from the H9/HTLV-III cell line having ATCC Accession No. CRL 8543;

wherein the single-stranded nucleic acid does not form a duplex with HTLV-I and HTLV-II nucleic acids under conditions of stringency for hybridization under which the single-stranded nucleic acid forms a duplex with the HIV-1 nucleic acid;

wherein the single-stranded nucleic acid consists of DNA;

wherein the duplex is outside of a mammalian cell;

wherein the duplex comprises a double-stranded region of at least 18 contiguous nucleotides and a single-stranded region on either side of the double-stranded region that is longer than the double-stranded region; and

wherein the duplex is bound to a solid support.

97. The composition of claim **96**, wherein the single-stranded nucleic acid comprises a nucleotide sequence which is part of an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or part of an HIV-1 long terminal repeat region.

98. The composition of claim **96**, wherein the single-stranded nucleic acid is selected from the group consisting of:

(i) a single-stranded nucleic acid consisting of from 18 to 103 nucleotides comprising a nucleotide sequence of at least 18 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 env open reading frame, an HIV-1 pol open reading frame or from an HIV-1 long terminal repeat region;

(ii) a single-stranded nucleic acid consisting of from 32 to 103 nucleotides comprising a nucleotide sequence of at least 32 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 env open reading frame, an HIV-1 pol open reading frame or from an HIV-1 long terminal repeat region;

(iii) a single-stranded nucleic acid consisting of from 20 to 100 nucleotides comprising a nucleotide sequence of at least 20 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 env open reading frame, an HIV-1 pol open reading frame or from an HIV-1 long terminal repeat region;

(iv) a single-stranded nucleic acid comprising a nucleotide sequence of at least about 32 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 env open reading frame, an HIV-1 pol open reading frame or from an HIV-1 long terminal repeat region; and

(v) a single-stranded nucleic acid comprising a nucleotide sequence of at least about 20 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 env open reading frame, an HIV-1 pol open reading frame or from an HIV-1 long terminal repeat region.

99. The composition of claim **96**, further comprising a compound selected from the group consisting of sodium saline citrate, formamide, and dextran sulfate.

100. The composition of claim **96**, wherein the single-stranded nucleic acid is randomly generated from an HIV-1 nucleic acid.

101. The composition of claim **96**, wherein the single-stranded nucleic acid comprises a label.

102. The composition of claim **96**, wherein the single-stranded nucleic acid comprises a non-HIV-1 DNA nucleotide sequence.

103. The composition of claim **96**, wherein the single-stranded nucleic acid is chemically made at least in part.

104. The composition of claim **96**, wherein the HIV-1 nucleic acid is a full-length HIV-1 nucleic acid.

105. The composition of claim **96**, wherein the HIV-1 nucleic acid is not a full-length HIV-1 nucleic acid.

106. A single-stranded nucleic acid of at least 18 contiguous nucleotides comprising a nucleotide sequence selected from the group consisting of:

(i) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB$_2$ having ATCC Accession No. 40231;

(ii) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB$_3$ having ATCC Accession No. 40232;

(iii) a nucleotide sequence of either strand of viral DNA from clone BH10 having ATCC Accession No. 40125;

(iv) a nucleotide sequence of either strand of viral DNA from clone BH5 having ATCC Accession No. 40126;

(v) a nucleotide sequence of either strand of viral DNA from clone BH8 having ATCC Accession No. 40127;

(vi) a nucleotide sequence of either strand of viral DNA from clone pHXB3 having ATCC Accession No. 67081;

(vii) a nucleotide sequence of either strand of viral DNA from clone pHXB-2D having ATCC Accession No. 67082;

(viii) a nucleotide sequence of either strand of viral DNA from *E. coli* clone X10-1 having ATCC Accession No. 67083; and

(ix) a Human Immunodeficiency Virus Type-1 (HIV-1) nucleotide sequence from the H9/HTLV-III cell line having ATCC Accession No. CRL 8543;

wherein the single-stranded nucleic acid does not form a duplex with HTLV-I and HTLV-II nucleic acids under conditions of stringency for hybridization under which the single-stranded nucleic acid forms a duplex with an HIV-1 nucleic acid;

wherein the single-stranded nucleic acid is outside of a mammalian cell and outside of a viral particle;

wherein the single-stranded nucleic acid consists of DNA; and

wherein the single-stranded nucleic acid is attached to a non-HIV-1 DNA nucleic acid through a covalent bond.

107. The single-stranded nucleic acid of claim **106**, wherein the nucleic acid is complementary to a sequence which is part of an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or part of an HIV-1 long terminal repeat region.

108. The single-stranded nucleic acid of claim **106**, wherein the single-stranded nucleic acid is selected from the group consisting of

(i) a single-stranded nucleic acid consisting of from 18 to 103 nucleotides comprising a sequence of at least 18 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region;

(ii) a single-stranded nucleic acid consisting of from 32 to 103 nucleotides comprising a sequence of at least 32 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region;

(iii) a single-stranded nucleic acid consisting of from 20 to 100 nucleotides comprising a sequence of at least 20 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region;

(iv) a single-stranded nucleic acid comprising a sequence of at least about 32 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region; and

(v) a single-stranded nucleic acid comprising a sequence of at least about 20 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region.

109. The single-stranded nucleic acid of claim **106**, wherein the single-stranded nucleic acid is randomly generated from an HIV-1 nucleic acid.

110. The single-stranded nucleic acid of claim **106**, wherein the single-stranded nucleic acid comprises a label.

111. The single-stranded nucleic acid of claim **106**, wherein the single-stranded nucleic acid is chemically made at least in part.

112. A composition comprising a duplex formed between:

(A) a single-stranded nucleic acid of between 18 and 103 contiguous nucleotides and comprising a nucleotide sequence selected from the group consisting of:

(i) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB$_2$ having ATCC Accession No. 40231;

(ii) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB$_3$ having ATCC Accession No. 40232;

(iii) a nucleotide sequence of either strand of viral DNA from clone BH10 having ATCC Accession No. 40125;

(iv) a nucleotide sequence of either strand of viral DNA from clone BH5 having ATCC Accession No. 40126;

(v) a nucleotide sequence of either strand of viral DNA from clone BH8 having ATCC Accession No. 40127;

(vi) a nucleotide sequence of either strand of viral DNA from clone pHXB3 having ATCC Accession No. 67081;

(vii) a nucleotide sequence of either strand of viral DNA from clone pHXB-2D having ATCC Accession No. 67082;

(viii) a nucleotide sequence of either strand of viral DNA from *E. coli* clone X10-1 having ATCC Accession No. 67083; and

(ix) a Human Immunodeficiency Virus Type-1 (HIV-1) nucleotide sequence from the H9/HTLV-III cell line having ATCC Accession No. CRL 8543; and

(B) an HIV-1 nucleic acid selected from the group consisting of:

(a) an HIV-1 nucleic acid comprising a nucleotide sequence encoding a full-length gag polypeptide or its complement;

(b) an HIV-1 nucleic acid comprising a nucleotide sequence encoding a full-length pol polypeptide or its complement;

(c) an HIV-1 nucleic acid comprising a nucleotide sequence encoding a full-length env polypeptide or its complement; and

(d) an HIV-1 nucleic acid comprising a nucleotide sequence for a long terminal repeat region comprising R and U$_3$ regions or their complements;

wherein the single-stranded nucleic acid of (A) does not form a duplex with HTLV-I and HTLV-II nucleic acids under conditions of stringency for hybridization under which the single-stranded nucleic acid of (A) forms a duplex with the HIV-1 nucleic acid of (B);

wherein the single-stranded nucleic acid of (A) consists of DNA;

wherein the duplex is outside of a mammalian cell and outside of a viral particle;

wherein the duplex comprises a double-stranded region of between 18 and 103 contiguous nucleotides and a single-stranded region on either side of the double-stranded region that is longer than the double-stranded region; and

wherein either the single-stranded nucleic acid or the duplex is bound to a solid support.

113. The composition of claim **112**, wherein the single-stranded nucleic acid comprises a nucleotide sequence which is part of an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or part of an HIV-1 long terminal repeat region.

114. The composition of claim **112**, wherein the single-stranded nucleic acid is selected from the group consisting of

(i) a single-stranded nucleic acid consisting of from 18 to 103 nucleotides comprising a sequence of at least 18 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region;

(ii) a single-stranded nucleic acid consisting of from 32 to 103 nucleotides comprising a sequence of at least 32 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region;

(iii) a single-stranded nucleic acid consisting of from 20 to 100 nucleotides comprising a sequence of at least 20 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region;

(iv) a single-stranded nucleic acid comprising a sequence of at least about 32 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region; and

(v) a single-stranded nucleic acid comprising a sequence of at least about 20 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region.

115. The composition of claim **112**, wherein the single-stranded nucleic acid is randomly generated from an HIV-1 nucleic acid.

116. The composition of claim **112**, wherein the single-stranded nucleic acid comprises a label.

117. The composition of claim **112**, wherein the single-stranded nucleic acid comprises a non-HIV-1 DNA nucleotide sequence.

118. The composition of claim **112**, wherein the single-stranded nucleic acid is chemically made at least in part.

119. The composition of claim **112**, wherein the single-stranded nucleic acid is bound to the solid support.

120. The composition of claim **112**, wherein the duplex is bound to the solid support.

121. The composition of claim **112**, wherein the HIV-1 nucleic acid is a full-length HIV-1 nucleic acid.

122. The composition of claim **112**, wherein the HIV-1 nucleic acid is not a full-length HIV-1 nucleic acid.

123. A composition comprising:

(A) a single-stranded nucleic acid of between 18 and 103 contiguous nucleotides and comprising a nucleotide sequence selected from the group consisting of:

(i) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_2 having ATCC Accession No. 40231;

(ii) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_3 having ATCC Accession No. 40232;

(iii) a nucleotide sequence of either strand of viral DNA from clone BH10 having ATCC Accession No. 40125;

(iv) a nucleotide sequence of either strand of viral DNA from clone BH5 having ATCC Accession No. 40126;

(v) a nucleotide sequence of either strand of viral DNA from clone BH8 having ATCC Accession No. 40127;

(vi) a nucleotide sequence of either strand of viral DNA from clone pHXB3 having ATCC Accession No. 67081;

(vii) a nucleotide sequence of either strand of viral DNA from clone pHXB-2D having ATCC Accession No. 67082;

(viii) a nucleotide sequence of either strand of viral DNA from *E. coli* clone X10-1 having ATCC Accession No. 67083; and

(ix) a Human Immunodeficiency Virus Type-1 (HIV-1) nucleotide sequence from the H9/HTLV-III cell line having ATCC Accession No. CRL 8543; and

(B) a compound selected from the group consisting of sodium saline citrate, formamide, and dextran sulfate;

wherein the single-stranded nucleic acid does not form a duplex with HTLV-I and HTLV-II nucleic acids under conditions of stringency for hybridization under which the single-stranded nucleic acid forms a duplex with an HIV-1 nucleic acid.

124. The composition of claim **123**, wherein the single-stranded nucleic acid comprises a sequence which is part of an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or part of an HIV-1 long terminal repeat region.

125. The composition of claim **123**, wherein the single-stranded nucleic acid is selected from the group consisting of:

(i) a single-stranded nucleic acid consisting of from 18 to 103 nucleotides comprising a sequence of at least 18 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region;

(ii) a single-stranded nucleic acid consisting of from 32 to 103 nucleotides comprising a sequence of at least 32 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region;

(iii) a single-stranded nucleic acid consisting of from 20 to 100 nucleotides comprising a sequence of at least 20 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region;

(iv) a single-stranded nucleic acid comprising a sequence of at least about 32 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region; and

(v) a single-stranded nucleic acid comprising a sequence of at least about 20 contiguous nucleotides from an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or from an HIV-1 long terminal repeat region.

126. The composition of claim **123**, wherein the single-stranded nucleic acid is randomly generated from an HIV-1 nucleic acid.

127. The composition of claim **123**, wherein the single-stranded nucleic acid comprises DNA.

128. The composition of claim **123**, wherein the single-stranded nucleic acid comprises RNA.

129. The composition of claim **123**, wherein the single-stranded nucleic acid is a cDNA.

130. The composition of claim **123**, wherein the single-stranded nucleic acid comprises a label.

131. The composition of claim **123**, wherein the single-stranded nucleic acid comprises a non-HIV-1 nucleotide sequence.

132. The composition of claim **123**, wherein the single-stranded nucleic acid is chemically made at least in part.

133. The composition of claim **123**, wherein the single-stranded nucleic acid is bound to a solid support.

134. A composition comprising a duplex formed between a Human Immunodeficiency Virus Type-1 (HIV-1) nucleic acid and a single-stranded nucleic acid comprising a nucleotide sequence selected from the group consisting of:

(i) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_2 having ATCC Accession No. 40231;

(ii) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_3 having ATCC Accession No. 40232;

(iii) a nucleotide sequence of either strand of viral DNA from clone BH10 having ATCC Accession No. 40125;

(iv) a nucleotide sequence of either strand of viral DNA from clone BH5 having ATCC Accession No. 40126;

(v) a nucleotide sequence of either strand of viral DNA from clone BH8 having ATCC Accession No. 40127;

(vi) a nucleotide sequence of either strand of viral DNA from clone pHXB3 having ATCC Accession No. 67081;

(vii) a nucleotide sequence of either strand of viral DNA from clone pHXB-2D having ATCC Accession No. 67082;

(viii) a nucleotide sequence of either strand of viral DNA from *E. coli* clone X10-1 having ATCC Accession No. 67083; and

(ix) an HIV-1 nucleotide sequence from the H9/HTLV-III cell line having ATCC Accession No. CRL 8543;

wherein the single-stranded nucleic acid does not form a duplex with HTLV-I and HTLV-II nucleic acids under conditions of stringency for hybridization under which the single-stranded nucleic acid forms a duplex with the HIV-1 nucleic acid;

wherein the duplex is outside of a mammalian cell and outside of an HIV-1 particle;

wherein the duplex comprises a double-stranded region and a single-stranded region on either side of the double-stranded region that is longer than the double-stranded region; and

wherein the single-stranded nucleic acid comprises a label.

135. The composition of claim **134**, wherein the single-stranded nucleic acid comprises a nucleotide sequence which is part of an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or part of an HIV-1 long terminal repeat region.

136. The composition of claim **134**, wherein the single-stranded nucleic acid comprises DNA.

137. The composition of claim **134**, wherein the single-stranded nucleic acid comprises RNA.

138. A composition comprising a duplex formed between a Human Immunodeficiency Virus Type-1 (HIV-1) nucleic acid and a single-stranded nucleic acid comprising a nucleotide sequence selected from the group consisting of:

(i) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_2 having ATCC Accession No. 40231;

(ii) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_3 having ATCC Accession No. 40232;

(iii) a nucleotide sequence of either strand of viral DNA from clone BH10 having ATCC Accession No. 40125;

(iv) a nucleotide sequence of either strand of viral DNA from clone BH5 having ATCC Accession No. 40126;

(v) a nucleotide sequence of either strand of viral DNA from clone BH8 having ATCC Accession No. 40127;

(vi) a nucleotide sequence of either strand of viral DNA from clone pHXB3 having ATCC Accession No. 67081;

(vii) a nucleotide sequence of either strand of viral DNA from clone pHXB-2D having ATCC Accession No. 67082;

(viii) a nucleotide sequence of either strand of viral DNA from *E. coli* clone X10-1 having ATCC Accession No. 67083; and

(ix) an HIV-1 nucleotide sequence from the H9/HTLV-III cell line having ATCC Accession No. CRL 8543;

wherein the single-stranded nucleic acid does not form a duplex with HTLV-I and HTLV-II nucleic acids under conditions of stringency for hybridization under which the single-stranded nucleic acid forms a duplex with the HIV-1 nucleic acid;

wherein the duplex is outside of a mammalian cell and outside of an HIV-1 particle;

wherein the duplex comprises a double-stranded region and a single-stranded region on either side of the double-stranded region that is longer than the double-stranded region; and

wherein either the duplex or the single-stranded nucleic acid is bound to a solid support.

139. The composition of claim **138**, wherein the single-stranded nucleic acid comprises a nucleotide sequence which is part of an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or part of an HIV-1 long terminal repeat region.

140. The composition of claim **138**, wherein the single-stranded nucleic acid comprises DNA.

141. The composition of claim **138**, wherein the single-stranded nucleic acid comprises RNA.

142. A composition comprising:

a compound selected from the group consisting of sodium saline citrate, formamide, and dextran sulfate; and

a duplex formed between a Human Immunodeficiency Virus Type-1 (HIV-1) nucleic acid and a single-stranded nucleic acid comprising a nucleotide sequence selected from the group consisting of:

(i) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_2 having ATCC Accession No. 40231;

(ii) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_3 having ATCC Accession No. 40232;

(iii) a nucleotide sequence of either strand of viral DNA from clone BH10 having ATCC Accession No. 40125;

(iv) a nucleotide sequence of either strand of viral DNA from clone BH5 having ATCC Accession No. 40126;

(v) a nucleotide sequence of either strand of viral DNA from clone BH8 having ATCC Accession No. 40127;

(vi) a nucleotide sequence of either strand of viral DNA from clone pHXB3 having ATCC Accession No. 67081;

(vii) a nucleotide sequence of either strand of viral DNA from clone pHXB-2D having ATCC Accession No. 67082;

(viii) a nucleotide sequence of either strand of viral DNA from *E. coli* clone X10-1 having ATCC Accession No. 67083; and

(ix) an HIV-1 nucleotide sequence from the H9/HTLV-III cell line having ATCC Accession No. CRL 8543;

wherein the single-stranded nucleic acid does not form a duplex with HTLV-I and HTLV-II nucleic acids under conditions of stringency for hybridization under which the single-stranded nucleic acid forms a duplex with the HIV-1 nucleic acid;

wherein the duplex is outside of a mammalian cell and outside of an HIV-1 particle;

wherein the duplex comprises a double-stranded region and a single-stranded region on either side of the double-stranded region that is longer than the double-stranded region.

143. The composition of claim **142**, wherein the single-stranded nucleic acid comprises a nucleotide sequence which is part of an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or part of an HIV-1 long terminal repeat region.

144. The composition of claim **142**, wherein the single-stranded nucleic acid comprises DNA.

145. The composition of claim **142**, wherein the single-stranded nucleic acid comprises RNA.

146. A composition comprising a duplex formed between a Human Immunodeficiency Virus Type-1 (HIV-1) nucleic acid and a single-stranded nucleic acid comprising a nucleotide sequence selected from the group consisting of:

(i) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_2 having ATCC Accession No. 40231;

(ii) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_3 having ATCC Accession No. 40232;

(iii) a nucleotide sequence of either strand of viral DNA from clone BH10 having ATCC Accession No. 40125;

(iv) a nucleotide sequence of either strand of viral DNA from clone BH5 having ATCC Accession No. 40126;

(v) a nucleotide sequence of either strand of viral DNA from clone BH8 having ATCC Accession No. 40127;

(vi) a nucleotide sequence of either strand of viral DNA from clone pHXB3 having ATCC Accession No. 67081;

(vii) a nucleotide sequence of either strand of viral DNA from clone pHXB-2D having ATCC Accession No. 67082;

(viii) a nucleotide sequence of either strand of viral DNA from *E. coli* clone X10-1 having ATCC Accession No. 67083; and

(ix) an HIV-1 nucleotide sequence from the H9/HTLV-III cell line having ATCC Accession No. CRL 8543;

wherein the single-stranded nucleic acid does not form a duplex with HTLV-I and HTLV-II nucleic acids under conditions of stringency for hybridization under which the single-stranded nucleic acid forms a duplex with the HIV-1 nucleic acid;

wherein the duplex is outside of a mammalian cell and outside of an HIV-1 particle;

wherein the duplex comprises a double-stranded region and a single-stranded region on either side of the double-stranded region that is longer than the double-stranded region; and

wherein the single-stranded nucleic acid is attached to a non-HIV-1 nucleic acid through a covalent bond.

147. The composition of claim **146**, wherein the single-stranded nucleic acid comprises a nucleotide sequence which is part of an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or part of an HIV-1 long terminal repeat region.

148. The composition of claim **146**, wherein the single-stranded nucleic acid comprises DNA.

149. The composition of claim **146**, wherein the single-stranded nucleic acid comprises RNA.

150. A nucleic acid comprising a nucleotide sequence selected from the group consisting of

(i) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_2 having ATCC Accession No. 40231;

(ii) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_3 having ATCC Accession No. 40232;

(iii) a nucleotide sequence of either strand of viral DNA from clone BH10 having ATCC Accession No. 40125;

(iv) a nucleotide sequence of either strand of viral DNA from clone BH5 having ATCC Accession No. 40126;

(v) a nucleotide sequence of either strand of viral DNA from clone BH8 having ATCC Accession No. 40127;

(vi) a nucleotide sequence of either strand of viral DNA from clone pHXB3 having ATCC Accession No. 67081;

(vii) a nucleotide sequence of either strand of viral DNA from clone pHXB-2D having ATCC Accession No. 67082;

(viii) a nucleotide sequence of either strand of viral DNA from *E. coli* clone X10-1 having ATCC Accession No. 67083; and

(ix) a Human Immunodeficiency Virus Type-1 (HIV-1) nucleotide sequence from the H9/HTLV-III cell line having ATCC Accession No. CRL 8543;

wherein the nucleic acid does not form a duplex with HTLV-I and HTLV-II nucleic acids under conditions of stringency for hybridization under which the nucleic acid forms a duplex with an HIV-1 nucleic acid; and

wherein the nucleic acid is covalently attached to a solid support.

151. The nucleic acid of claim **150**, wherein the nucleic acid comprises a nucleotide sequence which is part of an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or part of an HIV-1 long terminal repeat region.

152. The nucleic acid of claim **150**, wherein the nucleic acid comprises DNA.

153. The nucleic acid of claim **150**, wherein the nucleic acid comprises RNA.

154. A nucleic acid comprising a nucleotide sequence selected from the group consisting of

(i) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_2 having ATCC Accession No. 40231;

(ii) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_3 having ATCC Accession No. 40232;

(iii) a nucleotide sequence of either strand of viral DNA from clone BH10 having ATCC Accession No. 40125;

(iv) a nucleotide sequence of either strand of viral DNA from clone BH5 having ATCC Accession No. 40126;

(v) a nucleotide sequence of either strand of viral DNA from clone BH8 having ATCC Accession No. 40127;

(vi) a nucleotide sequence of either strand of viral DNA from clone pHXB3 having ATCC Accession No. 67081;

(vii) a nucleotide sequence of either strand of viral DNA from clone pHXB-2D having ATCC Accession No. 67082;

(viii) a nucleotide sequence of either strand of viral DNA from *E. coli* clone X10-1 having ATCC Accession No. 67083; and

(ix) a Human Immunodeficiency Virus Type-1 (HIV-1) nucleotide sequence from the H9/HTLV-III cell line having ATCC Accession No. CRL 8543;

wherein the nucleic acid does not form a duplex with HTLV-I and HTLV-II nucleic acids under conditions of stringency for hybridization under which the nucleic acid forms a duplex with an HIV-1 nucleic acid;

wherein the nucleic acid comprises a detectable label covalently attached to the nucleic acid; and

wherein the detectable label is not an additional nucleic acid.

155. The nucleic acid of claim **154**, wherein the nucleic acid comprises a nucleotide sequence which is part of an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or part of an HIV-1 long terminal repeat region.

156. The nucleic acid of claim **154**, wherein the nucleic acid comprises DNA.

157. The nucleic acid of claim **154**, wherein the nucleic acid comprises RNA.

158. A nucleic acid comprising a nucleotide sequence selected from the group consisting of

(i) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_2 having ATCC Accession No. 40231;

(ii) a nucleotide sequence of either strand of viral DNA from lambda bacteriophage λ-HXB_3 having ATCC Accession No. 40232;

(iii) a nucleotide sequence of either strand of viral DNA from clone BH10 having ATCC Accession No. 40125;

(iv) a nucleotide sequence of either strand of viral DNA from clone BH5 having ATCC Accession No. 40126;

(v) a nucleotide sequence of either strand of viral DNA from clone BH8 having ATCC Accession No. 40127;

(vi) a nucleotide sequence of either strand of viral DNA from clone pHXB3 having ATCC Accession No. 67081;

(vii) a nucleotide sequence of either strand of viral DNA from clone pHXB-2D having ATCC Accession No. 67082;

(viii) a nucleotide sequence of either strand of viral DNA from *E. coli* clone X10-1 having ATCC Accession No. 67083; and

(ix) a Human Immunodeficiency Virus Type-1 (HIV-1) nucleotide sequence from the H9/HTLV-III cell line having ATCC Accession No. CRL 8543;

wherein the nucleic acid does not form a duplex with HTLV-I and HTLV-II nucleic acids under conditions of stringency for hybridization under which the nucleic acid forms a duplex with an HIV-1 nucleic acid;

wherein the nucleic acid is outside of a mammalian cell and outside of a viral particle; and

wherein the nucleic acid is attached to a non-HIV-1 nucleic acid through a covalent bond.

159. The nucleic acid of claim **158**, wherein the nucleic acid comprises a nucleotide sequence which is part of an HIV-1 gag open reading frame, an HIV-1 pol open reading frame, an HIV-1 env open reading frame or part of an HIV-1 long terminal repeat region.

160. The nucleic acid of claim **158**, wherein the nucleic acid comprises DNA.

161. The nucleic acid of claim **158**, wherein the nucleic acid comprises RNA.

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